

77514

Delaval, Jan

From: Roark, Jessica
Sent: Wednesday, October 09, 2002 8:58 AM
To: Delaval, Jan
Subject: 09/780035

Jan,

Please search, including pending, for the following from 09/780035:

SEQ ID NO:70
SEQ ID NO:71.

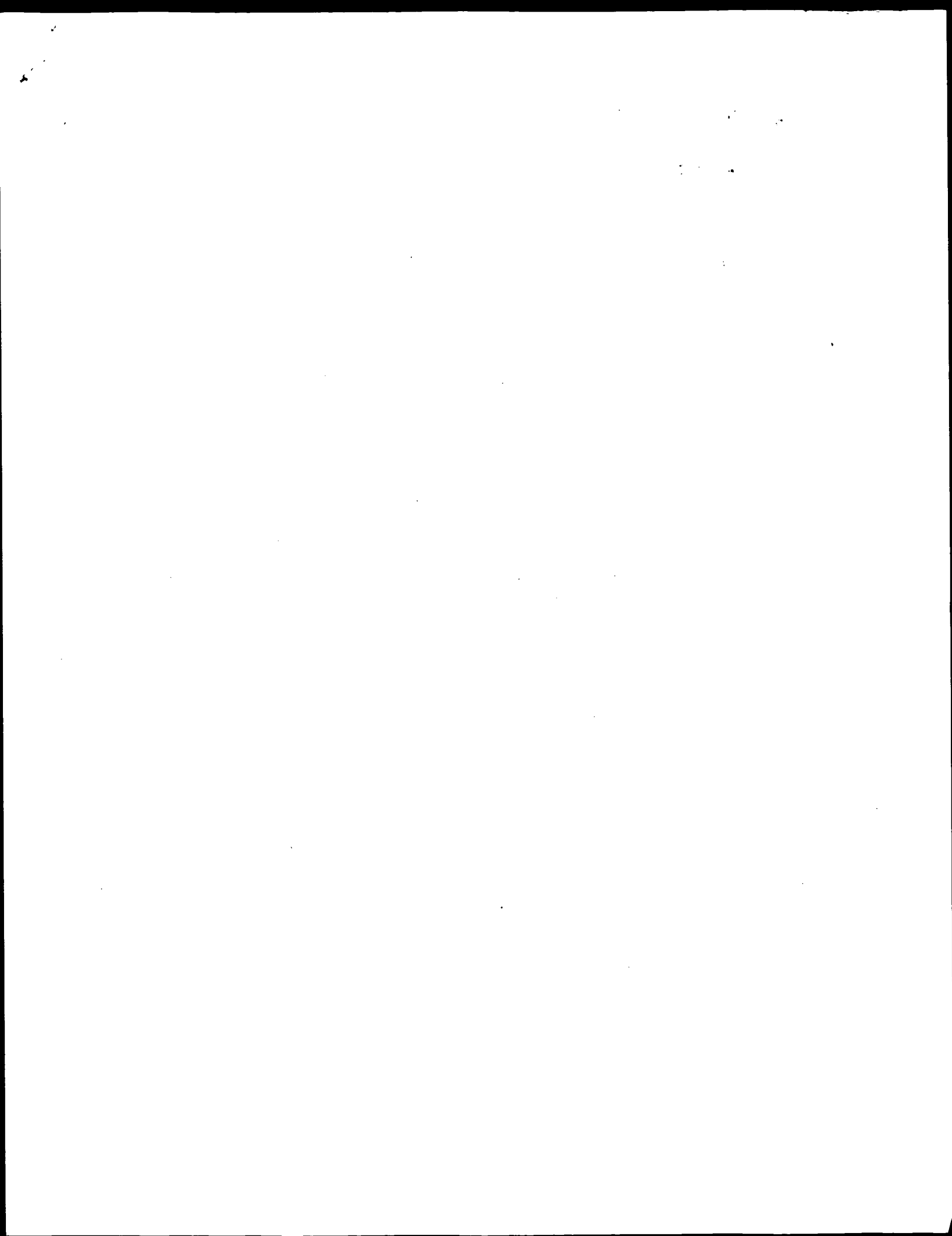
Results on paper please.

Thanks!

Jessica H. Roark

CM1 8A03
Mailbox 9E12
Art Unit 1644
703 605-1209

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov



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OM protein - protein search, using sw model

Run on: October 9, 2002, 09:15:09 ; Search time 84.17 Seconds

(without alignments)
87.096 Million cell updates/sec

Title: US-09-780-035-70

Perfect score: 339

Sequence: 1 YFGKLESLKSLVIRNLNDQVL.....FLIMYKDSQPRGMATISV 66

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
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9:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	339	100.0	66	22	AAG65356 Human interleukin-
2	339	100.0	157	17	AAR9564 Human interferon-g
3	339	100.0	157	17	AAR9558 Human mature inter
4	339	100.0	157	18	AAW15701 Interferon-gamma 1
5	339	100.0	157	18	AAW24258 Human protein for
6	339	100.0	157	19	AAW7158 Human interleukin-
7	339	100.0	157	19	AAW7158 Human interleukin-
8	339	100.0	157	19	AAW7158 Human interleukin-
9	339	100.0	157	19	AAW7158 Human interleukin-
10	339	100.0	157	19	AAW7158 Human interleukin-
11	339	100.0	157	19	AAW7158 Human interleukin-

12	339	100.0	157	19	AAW63810 Human IL-18 protei
13	339	100.0	157	19	AAW37741 IFN-gamma inducing
14	339	100.0	157	19	AAW52176 Interferon-gamma 1
15	339	100.0	157	20	AAW39799 Interleukin-18 rec
16	339	100.0	157	21	AAW44597 Human interleukin-
17	339	100.0	157	21	AAW53904 Sequence of a matu
18	339	100.0	157	21	AAW57570 Human interleukin
19	339	100.0	157	22	AAW06661 Human interleukin-
20	339	100.0	157	22	AAW82408 Human interleukin-
21	339	100.0	157	22	AAW65351 Human interleukin-
22	339	100.0	157	22	AAW65294 Human interleukin-
23	339	100.0	158	21	AAW85167 Human interleukin-
24	339	100.0	180	19	AAW48959 Human interleukin-
25	339	100.0	193	17	AAW95560 Wild-type human in
26	339	100.0	193	18	AAW31757 Human interleukin-9
27	339	100.0	193	18	AAW22047 Interferon gamma 1
28	339	100.0	193	19	AAW77082 Interleukin 18 act
29	339	100.0	193	19	AAW37740 Interleukin-gamma 1
30	339	100.0	193	19	AAW52172 Interleukin-gamma 1
31	339	100.0	193	19	AAW47429 Interleukin-gamma 1
32	339	100.0	193	19	AAW46592 Amino acid sequenc
33	339	100.0	193	21	AAW53908 Human interleukin-
34	339	100.0	193	22	AAW82409 Human interleukin-
35	339	100.0	193	22	AAW30541 A human IL-18 with
36	339	100.0	193	22	AAW63830 Amino acid sequenc
37	339	100.0	193	22	AAW72608 Macaca cynomolgus
38	339	100.0	157	19	AAW77080 Human interleukin
39	339	100.0	157	19	AAW77081 Human interleukin
40	339	100.0	157	19	AAW77082 Human interleukin
41	339	100.0	157	19	AAW77083 Human interleukin
42	339	100.0	157	19	AAW77084 Human interleukin
43	339	100.0	157	19	AAW77085 Human interleukin
44	339	100.0	157	19	AAW77086 Human interleukin
45	339	100.0	157	19	AAW77087 Human interleukin

ALIGNMENTS

RESULT 1	
AAW65356	standard, protein, 66 AA.
ID	AAW65356
XX	
AC	AAW65356
XX	
DT	30-NOV-2001 (first entry)
XX	
DE	Human interleukin-18 (IL-18) protein N-terminal fragment.
XX	
KW	IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;
KW	nocotropic; neurological; antiinflammatory; antiparkinsonian; cardiant;
KW	immunosuppressive; antidepressant; neuroleptic; hepatotropic.
XX	
OS	Homo sapiens.
XX	
PN	WO200158956-A2.
XX	
PD	16-AUG-2001.
XX	
PF	09-FEB-2001; 2001WO-US04170.
XX	
PR	10-FEB-2000; 2000US-0181608.
XX	
PA	(BADI) BASF AG.
XX	
PI	Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;
PI	Duncan AR, Brocklehurst SM, Mankovich J, Shortrock CP, Thompson JE;
PI	Lenard SN.
XX	
DR	WPI; 2001-550020/61.
XX	
PT	Novel antibodies and compounds capable of binding to human interleukin-18 useful for treating, e.g., inflammatory disorders,

XX WPI: 1996-252837/26.
DR N-PSDB; AAT32402.

PT DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
PT to treat and prevent, e.g. viral disease, malignancies and immune
PT disorders

XX Claim 1; Page 40; 48pp; English.

CC A novel human protein (AAR9558) induces interferon-gamma (IFN-gamma)
CC prodn. by immunocompetent cells. It enhances the cytotoxicity of
CC killer cells and/or induces the formation of killer cells (e.g.
CC NK cells, lymphokine-activating killer (LAK) cells, and cytotoxic
CC T-cells). Recombinant IFN-gamma inducer protein can be produced in
CC high yields using host cells, esp. Escherichia coli, transformed
CC with a vector carrying the encoding cDNA (AAT32402). It is useful
CC as an antiviral, antitumor, antibacterial, immunoregulatory and
CC blood platelet enhancing agent, and can be used in adoptive
CC immunotherapy. It is also used to raise monoclonal antibodies.
CC A full-length sequence is given in AAR95560.

XX Sequence 157 AA;

Query Match 100.0%; Score 339; DB 17; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.8e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNINDOVLFDGGRPLFEDMTDSCRDNPRTFTIISMWKDSQPRGM 60
DB 1 yfgklesklsvirindvlfidggnrplfedmtsdscrdnprftftlismykdsgprgm 60

QY 61 AVTISV 66
DB 61 avtlsv 66

RESULT 4
AAW15701
ID AAW15701 standard; protein: 157 AA.

AC AAW15701;

DT 26-JAN-1998 (first entry)

DE Interferon-gamma inducer protein.

KW Interferon-gamma, IFN-gamma; antiviral; antineoplastic; radiotherapy;
KW immunoregulatory; antitumor agent; chemotherapy; leukopenia;
KW thrombocytopenia; immunocompetent cell; asthma; hayfever;
KW rheumatism; interleukin; killer cell.

OS Homo sapiens.

Key Location/Qualifiers
FT Misc-difference 73 /label= Ile, Thr

PN EP67178-A1.

PD 09-APR-1997.

PF 26-SEP-1996; 96EP-0306997.

PR 20-SEP-1996; 96JP-0269105.

PR 26-SEP-1995; 95JP-0270725.

PR 29-FEB-1996; 96JP-0067434.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T;
XX

DR WPI: 1997-205381/19.

PT Human protein that induces interferon-gamma prodn. in
PT immuno:competent cells - useful for adoptive immuno:therapy of
PT tumours and as antimicrobial agent etc.

PS Claim 8; Page 20; 26pp; English.

CC The present sequence represents a novel protein from human cells, which
CC induces interferon-gamma (IFN gamma) production in immunocompetent cells.
CC This protein enhances cytotoxicity of killer cells and induces their
CC formation. It is used as an antineoplastic agent for antitumor
CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,
CC and in the treatment of atopic or immune system diseases, e.g. asthma,
CC hayfever or rheumatism. When formulated with interleukin-3, it is also
CC used to treat leukopenia and thrombocytopenia associated with
CC antitumor immunotherapy, this novel protein significantly improves the
CC immunotherapeutic effect of interleukin-2 (IL-2), compared with use of
CC IL-2 alone, either when administered to the patient (before
CC administration of IL-2) or by addition to the medium in which cells
CC (intended for return to the patient) are being grown.

XX Sequence 157 AA;

Query Match 100.0%; Score 339; DB 18; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.8e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNINDOVLFDGGRPLFEDMTDSCRDNPRTFTIISMWKDSQPRGM 60
DB 1 yfgklesklsvirindvlfidggnrplfedmtsdscrdnprftftlismykdsgprgm 60

QY 61 AVTISV 66
DB 61 avtlsv 66

RESULT 5
AAW24258

ID AAW24258 standard; protein: 157 AA.

AC AAW24258;

DT 15-OCT-1997 (first entry)

DE Human protein for induction of interferon-gamma.

KW Interferon-gamma; immunocompetent cell; malignant tumour;
KW viral disease; bacterial infection; immune disease.

OS Homo sapiens.

Key Location/Qualifiers
FT Misc-difference 73 /note= "Encoded by AYT"

PN JP09157180-A.

PD 17-JUN-1997.

PF 24-JAN-1996; 96JP-0028722.

PR 04-OCT-1995; 95JP-0279906.

PR 10-MAR-1995; 95JP-0078357.

PR 29-SEP-1995; 95JP-0274988.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI WPI: 1997-369391/34.
DR N-PSDB; AAT80209.
XX

PT A drug containing a polypeptide which induces interferon-gamma -
 PT useful for treating e.g. malignant tumours, viral, bacterial or
 PT immune diseases
 PS Claim 1; Page 9; 12pp; Japanese.
 XX
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 XX
 SQ Sequence 157 AA;
 XX
 Query Match 100.0%; Score 339; DB 18; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDGKRPLEFDMTSDCRDNAPRTIFILSMYKDSQPRGM 60
 1 yfgklesklsvirnlndqvlfidgknpplfedmtsdcrdnaprtilfilsmykdsqprgm 60
 Db 1 yfgklesklsvirnlndqvlfidgknpplfedmtsdcrdnaprtilfilsmykdsqprgm 60
 QY 61 AVTISV 66
 1 yfgklesklsvirnlndqvlfidgknpplfedmtsdcrdnaprtilfilsmykdsqprgm 60
 Db 61 avtislsv 66
 RESULT 6
 AAM77158
 ID AAM77158 standard; Protein; 157 AA.
 XX
 AC AAM77158;
 XX
 DT 26-NOV-1998 (first entry)
 XX
 DE Human Interleukin-18 protein (IL-18).
 XX
 KW Human; Interleukin-18 receptor; IL-18R; cytokine; signal transduction;
 KW Immune system; treatment; autoimmune; allergic disease;
 KW Immunosuppressant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 73 /note= "ile or thr"
 XX
 PN EP864585-A1.
 XX
 PD 16-SEP-1998.
 XX
 PF 23-DEC-1997; 97EP-0310517.
 XX
 PR 09-OCT-1997; 97JP-0291837.
 PR 12-MAR-1997; 97JP-0074697.
 PR 28-JUL-1997; 97JP-0215488.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Kurimoto M, Okura T, Torigoe K;
 XX
 DR WPI, 1998-469188/41.
 XX
 PT Interleukin-18 receptor polypeptide(s) - and corresponding DNA,
 PT which peptide compounds are useful for treating auto-immune or
 PT allergic diseases
 XX
 PS Disclosure; Pages 41-42; 51pp; English.
 XX
 CC The present sequence represents a human interleukin-18 (IL-18)
 CC polypeptide. Interleukin-18 is a type of cytokine which mediates signal
 CC transduction in immune systems. The interleukin-18 receptor polypeptide

CC can be used to neutralise interleukin-18 activity or to treat
 CC interleukin-18 receptor susceptible diseases, especially to treat
 CC auto-immune or allergic diseases or as an immunosuppressant. Conditions
 CC which may be treated include e.g. graft or organ rejection, pernicious
 CC anaemia, insulin-related diabetes, discoid lupus erythematosus,
 CC ulcerative colitis, hyperthyroidism, auto-immune hepatitis, systemic
 CC scleroderma, polymyositis, leukopenia, rheumatoid arthritis, HIV
 CC infections, asthma, atopic dermatitis, and pollinosis. The products may
 CC also be useful in the treatment of septic shock associated with
 CC IFN-alpha.
 XX
 SQ Sequence 157 AA;
 XX
 Query Match 100.0%; Score 339; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YFGKLESKLSVIRNLNDQVLFIDGKRPLEFDMTSDCRDNAPRTIFILSMYKDSQPRGM 60
 1 yfgklesklsvirnlndqvlfidgknpplfedmtsdcrdnaprtilfilsmykdsqprgm 60
 Db 1 yfgklesklsvirnlndqvlfidgknpplfedmtsdcrdnaprtilfilsmykdsqprgm 60
 QY 61 AVTISV 66
 1 yfgklesklsvirnlndqvlfidgknpplfedmtsdcrdnaprtilfilsmykdsqprgm 60
 Db 61 avtislsv 66
 RESULT 7
 AAM77077
 ID AAM77077 standard; peptide; 157 AA.
 XX
 AC AAM77077;
 XX
 DT 16-NOV-1998 (first entry)
 XX
 DE Human Interleukin 18.
 XX
 KW Human; Interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 KW osteoclastoma; Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 KW chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.
 XX
 OS Homo sapiens.
 XX
 PN EP861663-A2.
 XX
 PD 02-SEP-1998.
 XX
 PF 24-FEB-1998; 98EP-0301352.
 XX
 PR 25-FEB-1997; 97JP-0055468.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
 XX
 DR WPI, 1998-448964/39.
 DR N-PSDB; AAV48226.
 XX
 PT Use of interleukin-18 to inhibit osteoclast formation - in treatment
 PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 PT osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
 PT primary hyperthyroidism and osteoporosis
 XX
 PS Claim 4; Page 18; 56pp; English.
 XX
 CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 339; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YFGKLESKLSVIRNLNDQVLFIDGGRPLFEDMTDSDCRDNPRTIFITISMYKDSQPRGM 60
 |||
 DB 1 yfgklesklsvirnlndqylfidggnrpifedmtsdcrdnaprtilfifismykdsgprgm 60
 OY 61 AVTISV 66
 |||
 DB 61 avtlisv 66

RESULT 8

AAW77083
 ID AAW77083 standard; Peptide: 157 AA.

AC AAW77083;

DT 16-NOV-1998 (first entry)

DE Human interleukin 18 derivative 1.

XX Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 KW chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.

OS Homo sapiens.

XX EP861663-A2.

XX 02-SEP-1998.

XX 24-FEB-1998; 98EP-0301352.

XX 25-FEB-1997; 97JP-0055468.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

DR WPI; 1998-448964/39.

XX Use of interleukin-18 to inhibit osteoclast formation - in treatment
 PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 PT osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
 PT primary hyperthyroidism and osteoporosis

PS Disclosure; Page 30; 56pp; English.

CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.

XX Sequence 157 AA;

Query Match 100.0%; Score 339; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YFGKLESKLSVIRNLNDQVLFIDGGRPLFEDMTDSDCRDNPRTIFITISMYKDSQPRGM 60
 |||
 DB 1 yfgklesklsvirnlndqylfidggnrpifedmtsdcrdnaprtilfifismykdsgprgm 60
 OY 61 AVTISV 66
 |||
 DB 61 avtlisv 66

RESULT 9

AAW77085
 ID AAW77085 standard; Peptide: 157 AA.

AC AAW77085;

DT 16-NOV-1998 (first entry)

DE Human interleukin 18 derivative 3.

XX Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 KW chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.

OS Homo sapiens.

XX EP861663-A2.

XX 02-SEP-1998.

XX 24-FEB-1998; 98EP-0301352.

XX 25-FEB-1997; 97JP-0055468.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

DR WPI; 1998-448964/39.

XX Use of interleukin-18 to inhibit osteoclast formation - in treatment
 PT of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 PT osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
 PT primary hyperthyroidism and osteoporosis

PS Disclosure; Page 31; 56pp; English.

CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.

XX Sequence 157 AA;

Query Match 100.0%; Score 339; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YFGKLESKLSVIRNLNDQVLFIDGGRPLFEDMTDSDCRDNPRTIFITISMYKDSQPRGM 60
 |||
 DB 1 yfgklesklsvirnlndqylfidggnrpifedmtsdcrdnaprtilfifismykdsgprgm 60
 OY 61 AVTISV 66
 |||
 DB 61 avtlisv 66

RESULT 10

AAW48961
 ID AAW48961 standard; Peptide: 157 AA.

AC AAW48961;

DT 25-SEP-1998 (first entry)

DE Mutant human interferon-gamma inducing factor IGIF/MOTT2.

XX Interferon-gamma inducing factor; interferon-gamma; killer cell;

XX	antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
KW	hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
KM	osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
XX	
OS	Homo sapiens.
XX	Synthetic.
FT	Key
FT	Location/Qualifiers
FT	Misc-difference 68
FT	/note= "changed from Cys in wild-type to Ser in mutant"
XX	
PN	EP845530-A2.
PD	
XX	03-JUN-1998.
XX	
PF	28-NOV-1997; 97EP-0309632.
XX	
PR	14-NOV-1997; 97JP-0329715.
PR	29-NOV-1996; 96JP-0333037.
PR	21-JAN-1997; 97JP-0020906.
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX	
PI	Kurimoto M, Okamoto I, Yamamoto K;
XX	
DR	WPI; 1998-288747/26.
XX	
DR	N-PSDB; AAV32625.
XX	
PT	Mutants of interferon-gamma inducing polypeptide - useful as
XX	antitumour, antiviral, antimicrobial or anti-immunopathic agents
XX	
PS	Claim 5; page 41; 59pp; English.
XX	
CC	The present sequence represents the mutant human interferon-gamma
CC	inducing factor IGIF/MUT12. The wild-type human interferon-gamma
CC	factor sequence is shown in AAM48959. The invention provides for mutant
CC	human and mouse interferon-gamma inducing factors (IGIF) in which one
CC	or more cysteine residues are replaced with different residues at or
CC	away from the consensus sequences shown in AAM48956-W48958. The mutant
CC	IGIFs are capable of stimulating immunocompetent cells for the production
CC	of interferon-gamma and are claimed to be less toxic, more active and
CC	stable than the corresponding wild type interferon-gamma inducing
CC	factor. The mutant IGIFs are also claimed to enhance killer cell
CC	cytotoxicity and/or induce killer cell formation, and may therefore
CC	be useful as antitumour agents, antitumour immunotherapeutics, antiviral
CC	agents and antimicrobial agents. The mutant IGIFs are also claimed
CC	to be useful for treating hepatitis, acquired immunodeficiency syndrome
CC	(AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal
CC	carcinoma), rheumatism, osteoporosis and thrombopenia caused by
CC	radiation- and chemo-therapy.
XX	
SQ	Sequence 157 AA:
	Query Match 100.0%; Score 339; DB 19; Length 157;
	Best Local Similarity 100.0%; Pred. No. 2.8e-39;
	Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 YRGKESKLSVIRNLNDVLFIDGGRKRFEDMTSDSCRDNPRTFTIISMTKDSOPRCM 60
DB	1 YfGklesklsivirnlndvlfidggnrpfedmtsdscrdnaprtftlismykdsoprgm 60
OY	61 AVTISV 66
DB	61 avtisiv 66
	RESULT .11
	ID ' AAM48963 standard; peptide; 157 AA.
XX	
AC	AAM48963;

XX	25-SEP-1998	(first entry)
DT		
XX		
DE	Mutant human interferon-gamma inducing factor IGIF/MUT25.	
XX		
KW	Interferon-gamma inducing factor; interferon-gamma; killer cell;	
KW	antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;	
KW	hepatitis; malaria; tuberculosis; renal carcinoma; Rheumatism; AIDS;	
KW	osteoporosis; thrombopenia; acquired immunodeficiency syndrome.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference	127
FT		/note= "changed from Cys in wild-type to Ser in mutant"
XX		
PN	EP845530-A2.	
XX		
PD	03-JUN-1998.	
XX		
PF	28-NOV-1997;	97EP-0309632.
XX		
PR	14-NOV-1997;	97JP-0329715.
PR	29-NOV-1996;	96JP-0033037.
PR	21-JAN-1997;	97JP-0020906.
XX		
PA	(HAYB) HAYASHIBARA SETIBUTSU KAGAKU.	
XX		
PI	Kurimoto M, Okamoto I, Yamamoto K;	
XX		
DR	WPI: 1998-288747/26.	
XX		
DR	N-PSDB: AAV32627.	
PT	Mutants of interferon-gamma inducing polypeptide - useful as	
PT	antitumour, antiviral, antimicrobial or anti-immunopathic agents	
XX		
PS	Claim 5; pages 41-42; 59pp; English.	
XX		
CC	The present sequence represents the mutant human interferon-gamma	
CC	inducing factor IGIF/MUT25. The wild-type human interferon-gamma	
CC	nucleotide sequence is shown in AAW48959. The invention provides for mutant	
CC	human and mouse interferon-gamma inducing factors (IGIF) in which one or	
CC	more cysteine residues are replaced with different residues at or away	
CC	from the consensus sequences shown in AAW48956-W48958. The mutant IGIFs	
CC	are capable of stimulating immunocompetent cells for the production of	
CC	interferon-gamma and are claimed to be less toxic, more active and	
CC	stable than the corresponding wild type interferon-gamma inducing	
CC	factor. The mutant IGIFs are also claimed to enhance killer cell	
CC	cytotoxicity and/or induce killer cell formation, and may therefore	
CC	be useful as antitumour agents, antitumour immunotherapeutics, antiviral	
CC	agents and antimicrobial agents. The mutant IGIFs are also claimed	
CC	to be useful for treating hepatitis, acquired immunodeficiency syndrome	
CC	(AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal	
CC	carcinoma), rheumatism, osteoporosis and thrombopenia caused by	
CC	radiation- and chemo-therapy.	
XX		
XX		
SQ	Sequence	157 AA:
Query Match		
Best local Similarity 100.0%; Score 339; DB 19; Length 157;		
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 YEGKLESLKSVIRNLNDQVLFIDQGRPLFEDMTSDCDNAPRTIFITLSMKKDSQPRGM 60	
DB	1 YFGKLESKSLVIRNLNDQVLFIDQGRPLFEDMTSDCDNAPRTIFITLSMKKDSQPRGM 60	
QY	61 AAVTISV 66	
DB	61 AAVTISV 66	


```

RESULT 12
AAM63810
ID AAM63810 standard; protein; 157 AA.
XX
AC AAM63810;
XX
DT 28-SEP-1998 (first entry)
XX
DE Human IL-18 protein fragment.
XX
KW Interleukin-18; IL-18; human; treatment; autoimmune disease; antibody;
XX immunosuppressant; inhibitor; receptor protein; detection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1..157
FT /label= IL-18
FT /note= "partial sequence"
FT Misc-difference 73
FT /label= Thr or Ile
XX
PN EP850952-A1.
XX
PD 01-JUL-1998.
XX
PE 23-DEC-1997; 97EP-0310555.
XX
PR 28-JUL-1997; 97JP-0215490.
PR 26-DEC-1996; 96JP-0356426.
PR 21-FEB-1997; 97JP-0052526.
PR 06-JUN-1997; 97JP-0163490.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Kunikata T, Kurimoto M, Torigoe K, Ushio S;
XX WPI: 1998-335317/30.
XX
DR WPI: 1998-335317/30.
XX
PT New interleukin-18 receptor protein used to inhibit interleukin-18,
PT to treat autoimmune disease and as immunosuppressant - and new
PT monoclonal antibody and hybridoma used to detect interleukin-18
PT receptor protein
XX
PS Claim 5; Page 16; 35pp; English.
XX
CC This sequence represents a human interleukin-18 (IL-18) fragment which is
CC used in a method involved in neutralising IL-18 or to treat autoimmune
CC diseases or as an immunosuppressant using anti-IL-18 antibodies which
CC can inhibit IL-18. Such antibodies can also be used to detect the IL-18
CC receptor protein (labelled with an enzyme or a radioactive or fluorescent
CC substance). The protein is used to treat e.g. graft rejection, pernicious
CC anemia, atrophic gastritis, insulin-resistant diabetes, Wegener
CC granulomatosis, discoid lupus erythematosus, ulcerative colitis,
CC biliary cirrhosis, symmetrical ophthalmitis, hyperthyroidism, juvenile
CC onset type diabetes, Sjogren syndrome, autoimmune hepatitis, systemic
CC lupus erythematosus, myasthenia gravis, systemic scleroderma, systemic
CC periarthritis nodosa, multiple cold haemoglobinuria, polyomyelitis,
CC haemorrhagic, Basedow's disease, leukopenia, Behcet's disease, purpura
CC climacterium praecox, rheumatoid arthritis, rheumatopyra, chronic
CC thyroiditis, Hodgkin's disease, HIV, asthma, atopic dermatitis, allergic
CC nasitis, pollinosis, aptoxin-allergy and septic shock resulting from
CC production or administration of excessive gamma interferon (IFN-gamma).
XX
SQ Sequence 157 AA;

```

```

Query Match 100.0%; Score 339; DB 19; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.8e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YFGKLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCDRNAARTIFITSMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCDRNAARTIFITSMYKDSQPRGM 60
QY 61 AVTISV 66
DB 61 AVTISV 66

```

```

RESULT 13
AAM37741
ID AAM37741 standard; Protein; 157 AA.
XX
AC AAM37741;
XX
DT 07-JUL-1998 (first entry)
XX
DE IFN-gamma inducing active protein.
XX
KW Interferon-gamma inducing precursor peptide; IFN-gamma;
XX Interleukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;
XX antiviral agent; antitumour agent; immunopathy agent; antiseptic.
XX
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Misc-difference 73
FT /label= Ile, Thr
XX
PN EP821005-A2.
XX
PD 28-JAN-1998.
XX
PE 18-JUL-1997; 97EP-0305376.
XX
PR 31-JAN-1997; 97JP-0031474.
PR 25-JUL-1996; 96JP-0213267.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Kurimoto M, Tanimoto T;
XX WPI: 1998-088847/09.
XX
DR N-PSDB; AAV18906.
XX
PT Conversion of interferon-inducing polypeptide precursor to active
PT polypeptide - comprises use of interferon-1-beta-converting enzyme,
PT useful for, e.g. enhancing cytotoxicity by killer cells
XX
PS Claim 5; Page 15; 18pp; English.
XX
CC This is the amino acid sequence for the interferon-gamma (IFN-gamma)
CC inducing active protein which is cleaved to form the active mature
CC protein when it is in contact with interleukin-1-beta-converting
CC enzyme (ICE). The polypeptide is used for inducing, e.g. production
CC of IFN-gamma a useful biologically active substance, enhancing
CC cytotoxicity by, and inducing the formation of killer cells. The
CC polypeptide may potentially be used as an antiviral, antitumour and
CC immunopathy agent and as an antiseptic.
XX
SQ Sequence 157 AA;

```

```

Query Match 100.0%; Score 339; DB 19; Length 157;
Best Local Similarity 100.0%; Pred. No. 2.8e-39;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCDRNAARTIFITSMYKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDGGRPLFEDMTSDCDRNAARTIFITSMYKDSQPRGM 60
QY 61 AVTISV 66

```

DB 61 avl1sv 66

RESULT 14

AAW52176 standard; peptide; 157 AA.

AAW52176;

10-JUN-1998 (first entry)

Interferon-gamma inducing mature polypeptide.

Interferon-gamma; IFN-gamma; precursor; enzyme; cleavage.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 73 /label= Ile, Thr

EP819757-A2.

21-JAN-1998.

18-JUL-1997; 97EP-0305377.

30-MAY-1997; 97JP-0156062.

19-JUL-1997; 96JP-0207691.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Kurimoto M, Tanimoto T;

WPI; 1998-078838/08.

Polypeptide-processing enzyme - for preparing mature form of

interferon-inducing polypeptide

Claim 20; Page 17; 18pp; English.

This is an interferon-gamma (IFN-gamma) inducing polypeptide sequence.

This polypeptide induces IFN-gamma production in immunocompetent cells

[the polypeptide is not named but is described in JP 27198/96 and

193098/96]. An enzyme can convert the precursor form of this polypeptide

into this active form by cleaving a linkage between Asp at amino acid

position 36 and Tyr at amino acid position 37 of the precursor. The

enzyme can be obtained from a human haematopoietic cell and can be

inhibited by iodoacetamide and acetyl-L-tyrosyl-L-valyl-L-alanyl-L-

aspartyl-L-al. The enzyme can be used for cleaving a recombinant IFN-gamma

pro-polypeptide to form a mature polypeptide.

Sequence 157 AA;

DB 61 avl1sv 66

RESULT 15
AAV39799 standard; Protein; 157 AA.
ID AAV39799
XX

AC AAV39799;

29-NOV-1999 (first entry)

Interleukin-18 receptor protein sequence fragment.

Interleukin-18 receptor; IL-18; human; mouse; organ transplant rejection;

IL-18 receptor sensitive disease; immune reaction; therapy.

Mammalia.

Key Location/Qualifiers

Misc-difference 73 /note= "unspecified amino acid"

JP11240898-A.

07-SEP-1999.

12-MAR-1998; 96JP-0078549.

12-MAR-1997; 97JP-0074697.

28-JUL-1997; 97JP-0215488.

09-OCT-1997; 97JP-0291837.

26-DEC-1997; 97JP-0366908.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

WPI; 1999-555071/47.

New polypeptide - useful against interleukin-18 receptor sensitive

diseases

Disclosure; Page 37; 41pp; Japanese.

This sequence is a fragment of an interleukin-18 receptor (IL-18R) of the

invention. The IL-18R sequences were isolated from human and mouse. The

sequences can be used in drugs for treating IL-18 receptor sensitive

disease, especially effective for the relief of rejection accompanied to

organ transplantation and for the treatment and the prevention of various

diseases caused by excessive immune reaction.

Sequence 157 AA;

DB 61 avl1sv 66

Search completed: October 9, 2002, 11:02:44
Job time: 6455 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2002, 11:03:39 ; Search time 40.26 Seconds
(without alignments)
63.475 Million cell updates/sec

Title: US-09-780-035-70

Perfect score: 339
Sequence: 1 YFGKLSKLSVIRNLENDVLT.....FIISMYKDSQPRGMATVISV 66

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	339	100.0	193	IL18_HUMAN	Q14116 homo sapien
2	277	81.7	193	IL18_HORSE	O9XSG7 equus caball
3	276	81.4	193	IL18_BOVIN	O9LUT3 bos taurus
4	276	81.4	193	IL18_CANFA	O9XST0 canis famill
5	267	78.8	192	IL18_PIG	O19073 sus scrofa
6	186.5	55.0	192	IL18_MOUSE	P70380 mus musculu
7	186	54.9	194	IL18_RAT	P97636 rattus norv
8	70	20.6	1772	MSPI_PLAYO	P13828 plasmodium
9	61.5	18.1	375	YGC5_CAEEL	Q18610 caenorhabdi
10	61.5	18.1	919	RPO2_CAPVK	P16716 capripoxvir
11	61.5	18.1	950	CDAD_HUMAN	O9Y510 homo sapien
12	60.5	17.8	868	CHVA_AGRVU	P18768 agrobacteri
13	59	17.4	867	RPO_BVDV1	P29044 barley yell
14	59	17.4	867	RPO_BVDV	P29045 barley yell
15	59	17.4	1507	CADE_DROME	O24298 drosophila
16	58.5	17.3	695	FEAL_SCHPO	O09740 schizosacch
17	57.5	17.0	372	YUGP_HAEIN	Q45333 haemophilus
18	56.5	16.7	894	Y330_CAEEL	Q19338 caenorhabdi
19	55.5	16.4	542	RESE_BACSU	P35161 bacillus su
20	55.5	16.4	983	YOG4_CAEEL	O09499 caenorhabdi
21	55.5	16.4	1067	IMB4_SCHPO	O60100 schizosacch
22	55	16.2	749	STAI_MOUSE	P42225 mus musculu
23	55	16.2	800	KINA_YEAST	O01819 saccharomyc
24	55	16.2	2555	PPS3_BACSU	P39847 bacillus su
25	54.5	16.1	373	LEF3_NAPOV	O65365 orgyia pseu
26	54.5	16.1	669	VHRP_COMPX	P12932 compox viru
27	54	15.9	152	Y396_MYCPN	P53327 mycoplasma
28	54	15.9	321	PDR_BURCE	P33164 burkholderi
29	54	15.9	339	YB30_ARATH	O82314 arabidopsis
30	54	15.9	375	MASF_MOUSE	P70124 mus musculu
31	54	15.9	1044	YAF3_SCHPO	O09857 schizosacch
32	54	15.9	1164	RPO2_COMPX	P17474 compox viru
33	54	15.9	1164	RPO2_VACCV	P19798 vaccinia vi

ALIGNMENTS

RESULT	ID	IL18_HUMAN	STANDARD	PRT	193 AA
AC	Q14116	075599;			
DT	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	01-MAR-2002	(Rel. 41, Last annotation update)			
DE	Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)				
DE	(IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).				
GN	IL18 OR IGIF.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RX	MEDLINE=96247646; PubMed=8666798;				
RA	Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,				
RA	Tanabe F., Konishi K., Micallef M., Fujii M., Torisoe K., Tanimoto T.,				
RA	Fukuda S., Ikeda M., Okamura H., Kurimoto M.,				
RT	"Cloning of the cDNA for human IFN-gamma-inducing factor, expression				
RT	in Escherichia coli, and studies on the biologic activities of the				
RT	protein.";				
RL	J. Immunol. 156:4274-4279(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Yong D., Guixia D., Lihua H., Haitao W.,				
RT	"Cloning and sequencing of the cDNA for precursor hIL-18.";				
RT	Submitted (Jul-1998) to the EMBL/Genbank/DBJ databases.				
RL	Submitted (Jul-2001) to the EMBL/Genbank/DBJ databases.				
RN	[4]				
RP	SEQUENCE OF 2-193 FROM N.A.				
RC	TISSUE=peripheral blood;				
RA	Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.,				
RL	Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.				
CC	- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS				
CC	AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I				
CC	CELLS.				
CC	- SUBCELLULAR LOCATION: Secreted.				
CC	- SIMILARITY: BELONGS TO THE IL-18 FAMILY.				
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	EMBL: D49950; BAA08706.1; -				
DR	EMBL: AF077611; AAC27787.1; -				

34	54	15.9	1164	1	RPO2_VARY	P33811 variola vir
35	54	15.9	1950	1	UBR1_YEAST	P19812 saccharomyc
36	53.5	15.8	317	1	YQ35_CAEEL	O09456 caenorhabdi
37	53.5	15.8	402	1	CAR1_CANFA	P32951 candida par
38	53.5	15.8	679	1	GR78_KLULA	P22010 kluyveromyc
39	53.5	15.8	700	1	NOMA_DROME	O04047 drosophila
40	53.5	15.8	1228	1	ECM_HUMAN	O13201 homo sapien
41	53	15.6	439	1	Y811_METJA	O58221 methanococ
42	53	15.6	638	1	LIK2_RAT	P53670 rattus norv
43	53	15.6	664	1	DEL1_CAEEL	O19038 caenorhabdi
44	53	15.6	714	1	CAN1_HUMAN	P07384 homo sapien
45	53	15.6	867	1	RPO_BVDV	P09505 barley yell

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DR EMBL: AY044641; AAK95950.1; -
DR EMBL: U90434; AAB50010.1; -
DR MIM: 600953; -
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
FT CONFLICT 66 66 F -> L (IN REF. 2).
FT CONFLICT 86 86 S -> R (IN REF. 2).
FT CONFLICT 191 191 N -> S (IN REF. 2).
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788B55 CRC64;

Query Match 100.0%; Score 339; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 6; 6e-34;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGLESKLSVIRNLNDQVLFIDGNGRPLFEDMTSDCDRNAPRTIFIIISMVKDSQPRGM 60
DB 37 YFGLESKLSVIRNLNDQVLFIDGNGRPLFEDMTSDCDRNAPRTIFIIISMVKDSQPRGM 96
QY 61 AVTISV 66
DB 97 AVTISV 102

RESULT 2
ID IL18_HORSE STANDARD; PRT; 193 AA.
AC O9XSO7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
DE IL18 OR IGIF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
RX (1)
RP SEQUENCE FROM N.A.
RA Nicolson L., Penha-Goncalves M.N., Keanle J.L., Logan N.A.,
RA Argyle D.J., Onions D.E.;
RA "Nucleotide sequence of equine interleukin 12 and 18 cDNAs.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
-----
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CC or send an email to license@sib-sib.ch).
-----
CC EMBL: Y11131; CAA72013.1; -.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAC CRC64;

Query Match 81.7%; Score 277; DB 1; Length 193;
Best Local Similarity 78.8%; Pred. No. 2e-26;
Matches 52; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 YFGLESKLSVIRNLNDQVLFIDGNGRPLFEDMTSDCDRNAPRTIFIIISMVKDSQPRGM 60
DB 37 YFGLESKLSVIRNLNDQVLFIDGNGRPLFEDMTSDCDRNAPRTIFIIISMVKDSQPRGM 60
QY 61 AVTISV 66
DB 97 AVTISV 102

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DB 37 YFGLEPKLSITIRNLNDQVLFIDGNGRPLFEDMDPDSCTDNPQTIVFIYMKDSLTRGL 96
QY 61 AVTISV 66
DB 97 AVTISV 102

RESULT 3
ID IL18_BOVIN STANDARD; PRT; 193 AA.
AC O9TU73;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).
DE IL18.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RX (1)
RP SEQUENCE FROM N.A.
RA MEDLINE-20012648; PubMed-10547157;
RA Shoda L.K., Zarlenga D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
-----
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CC or send an email to license@sib-sib.ch).
-----
CC EMBL: AF124789; AAF08686.1; -.
DR InterPro: IPR000975; Interleukin_1.
DR SMART: SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 81.4%; Score 276; DB 1; Length 193;
Best Local Similarity 80.3%; Pred. No. 2.6e-26;
Matches 53; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 YFGLEPKLSITIRNLNDQVLFIDGNGRPLFEDMDPDSCTDNPQTIVFIYMKDSLTRGL 96
DB 37 HFGLEPKLSITIRNLNDQVLFIDGNGRPLFEDMDPDSCTDNPQTIVFIYMKDSLTRGL 96
QY 61 AVTISV 66
DB 97 AVTISV 102

RESULT 4
ID IL18_CANFA STANDARD; PRT; 193 AA.
AC O9XSR0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2002, 11:03:04 ; Search time 105.02 Seconds

(without alignments)
108.719 Million cell updates/sec

Title: US-09-780-035-70

Sequence: 1 YFGKLESKLSVIRNLNDQVL.....FIISMKDSQPRGMATVTSV 66

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriophage:*
17: SP-archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	334	99.5	193	4	Q96KJ8
2	330	97.3	193	6	Q9BG15
3	276	81.4	84	6	Q95LE7
4	276	81.4	178	6	Q9WZL8
5	275	81.1	193	6	Q9GLT9
6	271	79.9	192	6	Q9SM33
7	267	78.8	192	6	Q9N1P7
8	204	60.2	45	4	Q9N049
9	155.5	45.9	196	11	Q91Z66
10	78.5	23.2	211	13	Q98S01
11	68.5	20.2	198	13	Q918D2
12	66.5	19.6	304	15	Q97685
13	65.5	19.3	1044	3	Q94173
14	64	18.9	366	16	Q66840
15	63.5	18.7	441	4	Q9HCV3
16	63	18.6	407	10	Q9C965

17	63	18.6	1766	5	Q25668
18	62	18.6	1785	5	Q25685
19	62	18.3	320	10	Q9FG29
20	61.5	18.1	1156	12	Q91MP7
21	61	18.0	1408	17	Q27357
22	60.5	17.8	718	4	Q9NVJ0
23	60.5	17.8	853	4	Q9NSG2
24	59	17.4	381	3	Q43031
25	59	17.4	532	12	Q65871
26	59	17.4	532	12	Q65876
27	59	17.4	867	12	Q91Z62
28	59	17.4	913	11	Q88195
29	59	17.4	979	11	Q91Y11
30	58.5	17.3	364	16	Q9PM33
31	58.5	17.3	419	17	Q973T1
32	58.5	17.3	713	11	Q91Y19
33	58	17.1	334	10	Q9ZSB9
34	57.5	17.0	747	3	Q42977
35	57.5	17.0	1026	3	Q74669
36	57	16.8	83	9	Q9ZX89
37	57	16.8	297	12	Q9DVT8
38	57	16.8	327	10	Q9LP17
39	57	16.8	617	11	Q54776
40	57	16.8	638	11	Q54785
41	57	16.8	1092	3	Q9UVY2
42	56.5	16.7	98	11	Q9QWV3
43	56.5	16.7	520	5	Q21385
44	56.5	16.7	644	4	Q9Y2K1
45	56.5	16.7	647	16	Q84627

ALIGNMENTS

Result 1
Q96KJ8 PRELIMINARY; PRT; 193 AA.
AC Q96KJ8;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE INTERLEUKIN 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying P., Jianxin L.;
RT "Cloning of Mutant Human Interleukin 18 cDNA."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380360; AAK57024.1; -
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;

Query Match 98.5%; Score 334; DB 4; Length 193;
Best Local Similarity 98.5%; Pred. No. 1.8e-34;
Matches 65; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFDGQNRPLFEDMTDSDCRNAPPTITITISMYSKDSQPRGM 60
Db |||||||

QY 37 YFGKLESKLSVIRNLNDQVLFDGQNRPLFEDMTDSDCRNAPPTITITISMYSKDSQPRGM 96
Db |||||||

QY 61 AVTTSV 66
Db |||||||

RESULT 2
Q9BG15 PRELIMINARY; PRT; 193 AA.
ID Q9BG15;
AC Q9BG15;
DT 01-JUN-2001 (TREMblrel. 17, Created)

Q25668 plasmodium
Q25685 plasmodium
Q9FG29 arabidopsis
Q91MP7 lumpy skin
Q9NVJ0 methanother
Q9NSG2 homo sapien
Q43031 schizosach
Q65871 barley yell
Q65876 barley yell
Q91Z62 barley yell
Q88195 mus musculu
Q91Y11 mus musculu
Q9PM33 campylobact
Q973T1 sulfolobus
Q91V19 mus musculu
Q9ZSB9 arabidopsis
Q42977 schizosach
Q74669 pneumocysti
Q9ZX89 bacterioph
Q9DVT8 pluteella xy
Q9LP17 arabidopsis
Q54776 mus musculu
Q54785 mus musculu
Q9UVY2 pneumocysti
Q9QWV3 mus musculu
Q21385 caenorhabdi
Q9Y2K1 homo sapien
Q84627 chlamydia t

DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE INTERLEUKIN-18.
GN IL18.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Crniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca
OX NCBI_taxid=9344;
RN [1]
RP
RP SEQUENCE FROM N.A.
RA MEDLINE=21229850; PubMed=11331040;
RA Glavedoni L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
RA Hodara V.L.;
RT "Expression of the Interleukin-18 Gene from Rhesus Macaque by the
RT Simian Immunodeficiency Virus Does Not Result In Increased Viral
RT Replication.";
RT J. Interferon Cytokine Res. 21:173-180(2001).
RL EMBL: AF303732; AAK13416.1;
SQ SEQUENCE 193 AA; 22325 MW; B2MD2C033BB05BE CRC64;

	Query Match	97.3%	Score 330;	DB 6;	Length 193;	
	Best Local Similarity	95.5%;	Pred. No. 5.7e-34;			
	Matches	63; Conservative	2; Mismatches	1; Indels	0; Gaps	0.
Oy	1 YFGKLESKLTVIRNLNDQVLFIDCGNRPLFEDMTSDCDRNAPRITFIISMYKDSQPRGM	60				
	: : :					
Dd	37 YFGKLESKITLRNLNDQVLFIDCGNRPLFEDMTSDCDNA PRITFIITNMKIDSQPRGM	96				
Oy	61 AVTISY	66				
Dd	97 AVAISY	102				

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Query Match      81.4%; Score 276; DB 6; Length 84;
Best Local Similarity 78.8%; Pred. No. 1,6e-27;
Matches      52; Conservative      7; Mismatches      7; Indels      0; Gaps      0

QY      1 YFGLESKSLVIRNLNDQVLFIDQGNRPLEFEDMTSDSCDRNAERTTFTISMRYDSQPRGM 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      5 YGKLEPKRSTIRNLNDQVLFVNEGQNPVEFEDNPBDDCIGNAHRTFTFTMYKDSLTRLG 64

QY      61 AVTISY 66
      |||||
Db      65 AVTISY 70

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RESULT	4		
09MZL8			
ID	09MZL8	PRELIMINARY;	PRT; 178 AA.
AC	09MZL8;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, last sequence update)		
DT	01-JUN-2001 (TrEMBLrel. 17, last annotation update)		
DE	INTERLEUKIN-18 (FRAGMENT).		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Bovinae; Bos.		
OX	NCBI_Taxid=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=KIDNEY, LIVER, BLOOD MONONUCLEAR CELLS;		
RA	Olsen S.C., Lee I.K., Mwangi S.M., Kehrl M., Bolin C.A.;		
RT	"Cloning of bovine interleukin-18, expression in <i>Escherichia coli</i> , and		
RT	characterization of the biologic activities of the recombinant		
RT	cytokine.";		
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; AF173175; AAF8963.1; "		
DR	InterPro; IPR000975; Interleukin_1.		
DR	SMART; SM00125; IL1; 1.		
FT	NON_TER	1	
FT	NON_TER	178	178
SO	SEQUENCE	178 AA; 20631 MW; 816D6B2B88ACB497 CRC64;	

Query Match	81.4%	Score 276;	DB 6;	Length 178;
Best Local Similarity	80.3%;	Pred. No. 3.7e-27;		
Matches	53;	Conservative	7;	Mismatches 6; Indels 0; Gaps 0;
Qy	1	YEGKESKLSVIRINDQVLEFDGCRNPFLFEDMTSDCDRNAPRTIFIIISMYKDSQPRGM	60	
	:		11:	
Db	22	HGKLEPKSLIRINDQVLEFDGCRNPFLFEDMTSDCDRNAPRTIFIIISMYKDSQPRGM	81	
Qy	61	AVTISY	66	
	:			
Db	82	AVTISY	87	

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Query Match 81.1%; Score 275; DB 6; Length 133;
Best Local Similarity 80.3%; Pred. No. 5.5e-27;
Matches 53; Conservative 6; Mismatches 7; Indels 0; Gaps 0.
QY 1 YRGKLESKISVLRNLDVLFIDGGRPLFEDMTSDCDNAPRTIFILSMYKDSQPRGM 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 09:17:14 ; Search time 39.04 Seconds
(without alignments)
41.293 Million cell updates/sec

Title: US-09-780-035-70

Perfect score: 339

Sequence: 1 YFGKLESLKLVIRNLNDQYL.....FLIMYKDSQPRGMATISV 66

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5a_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5b_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5a_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/5b_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	339	100.0	157	2	US-08-896-605A-6
2	339	100.0	157	2	US-08-896-605A-6
3	339	100.0	157	3	US-08-884-324-1
4	339	100.0	157	3	US-08-996-338-26
5	339	100.0	157	4	US-08-558-818-1
6	339	100.0	157	4	US-08-974-469A-1
7	339	100.0	157	4	US-08-832-180-1
8	339	100.0	157	4	US-08-832-180-1
9	339	100.0	157	4	US-08-832-180-1
10	339	100.0	193	2	US-08-896-605A-2
11	339	100.0	193	2	US-08-896-605A-2
12	259	76.4	50	4	US-08-832-180-9
13	186.5	55.0	157	2	US-08-502-535B-2
14	186.5	55.0	157	2	US-08-908-005A-2
15	186.5	55.0	157	3	US-08-996-338-27
16	186.5	55.0	157	4	US-08-558-818-7
17	186.5	55.0	157	4	US-08-974-469A-7
18	186.5	55.0	157	4	US-08-832-180-8
19	186.5	55.0	157	4	US-08-832-180-11
20	186.5	55.0	157	4	US-09-253-523-2
21	186.5	55.0	157	4	US-09-251-911-2
22	71	20.9	13	4	US-08-832-198-4
23	63	18.6	13	4	US-08-832-198-4
24	55	16.2	749	2	US-08-369-796-8
25	55	16.2	749	2	US-08-852-091-8
26	55	16.2	749	2	US-08-820-754-8
27	55	16.2	749	3	US-08-956-652-8

28	55	16.2	749	3	US-08-956-869-8	Sequence 8, Appl1
29	55	16.2	749	3	US-09-012-710-7	Sequence 7, Appl1
30	55	16.2	749	3	US-08-948-547-8	Sequence 8, Appl1
31	55	16.2	749	4	US-09-556-273-7	Sequence 7, Appl1
32	55	16.2	749	4	US-08-956-653A-8	Sequence 8, Appl1
33	55	16.2	749	5	PCT-US95-17025-8	Sequence 115, App
34	54.5	16.1	616	1	US-08-453-695A-115	Sequence 115, App
35	54.5	16.1	616	1	US-08-268-161A-115	Sequence 115, App
36	54.5	16.1	616	2	US-08-453-702A-115	Sequence 115, App
37	54.5	16.1	616	4	US-09-099-639-115	Sequence 115, App
38	54.5	16.1	616	4	PCT-US95-08071-115	Sequence 115, App
39	54.5	16.1	616	4	US-09-004-838-88	Sequence 115, App
40	54.5	16.1	1366	4	US-09-004-838-88	Sequence 115, App
41	53.5	15.8	679	1	US-08-441-139-5	Sequence 115, App
42	53	15.6	119	4	US-08-680-726A-62	Sequence 88, Appl
43	53	15.6	119	4	US-09-092-409-62	Sequence 62, Appl
44	53	15.6	149	1	US-08-602-010A-18	Sequence 18, Appl
45	53	15.6	149	1	US-08-680-726A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-896-605A-6
: Sequence 6, Application US/08896605A
: Patent No. 5879942
: GENERAL INFORMATION:
: APPLICANT: TANIMOTO, Tadao
: APPLICANT: KURIMOTO, Masashi
: TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESS: BROWDY AND NEWMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/896,605A
: FILING DATE: 18 July 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 207,691/1996
: FILING DATE: 19-JUL-1996
: APPLICATION NUMBER: JP 156,062/1997
: FILING DATE: 30-MAY-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: TANIMOTO-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 157 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-896-605A-6

Query Match 100.0%; Score 339; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. NO. 5.5e-40;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFDMTSDCDRNAPRITFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFDMTSDCDRNAPRITFIISMVKDSQPRGM 60
QY 61 AVTISV 66
DB 61 AVTISV 66

RESULT 2
US-08-896-501A-4

; Sequence 4, Application US/08896501A
; Patent No. 5891663
; GENERAL INFORMATION:
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,501A
; FILING DATE: 18-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 213,267/1996
; FILING DATE: 25-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 31,474/1997
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TANIMOTO-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-896-501A-4

Query Match 100.0%; Score 339; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.5e-40;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFDMTSDCDRNAPRITFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFDMTSDCDRNAPRITFIISMVKDSQPRGM 60
QY 61 AVTISV 66
DB 61 AVTISV 66

RESULT 3
US-08-884-324-1
; Sequence 1, Application US/08884324

; Patent No. 6060283
; GENERAL INFORMATION:
; APPLICANT: Takano, OKURA
; APPLICANT: Kakuji TORIGOE
; APPLICANT: Masashi KURIMOTO
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
; TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,324
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 185,305/96
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: OKURA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-884-324-1

Query Match 100.0%; Score 339; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.5e-40;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFDMTSDCDRNAPRITFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLEFDMTSDCDRNAPRITFIISMVKDSQPRGM 60
QY 61 AVTISV 66
DB 61 AVTISV 66

RESULT 4
US-08-996-338-26

; Sequence 26, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: OKURA, Takano, Masashi
; TITLE OF INVENTION: POLYPEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 09:19:24 ; Search time 56.97 Seconds

(without alignments)
111.320 Million cell updates/sec

Title: US-09-780-035-70

Sequence: 1 YFGKLESLKSLVIRNLNDQVL.....FLISMVKDSQPRGMATVISV 66

Scoring table: BIOSIM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	186.5	55.0	192	2	S60226 cytokine IGIF - mo
2	70	20.6	680	2	A28121 major mezozoite su
3	70	20.6	1772	2	A45532 major mezozoite su
4	64	18.9	366	1	D70351 probable hexosyltr
5	63	18.6	407	2	G96835 probable RING zinc
6	63	18.6	1785	2	A45564 major mezozoite su
7	61.5	18.1	375	2	T29568 DNA-directed RNA p
8	61.5	18.1	919	1	RNVZCA cell surface glyco
9	61	18.0	1408	2	H69068 beta-1,2-glucan ex
10	60.5	17.8	588	1	VXAGCA beta-(1->2) glucan
11	60.5	17.8	598	2	E97686 beta-(1->2) glucan
12	60.5	17.8	598	2	AG2911 beta-(1->2) glucan
13	59	17.4	381	2	T40341 RNA-directed RNA p
14	59	17.4	532	1	RNVOC2 RNA-directed RNA p
15	58.5	17.3	364	2	A81261 probable fructos
16	58.5	17.3	696	2	T11674 glutamine--fructos
17	58.5	17.3	1159	2	B98198 hypothetical prote
18	58.5	17.3	1159	2	AH3088 hypothetical prote
19	58	17.1	334	2	T04198 Icmf [imported] -
20	57.5	17.0	372	2	A64176 hypothetical prote
21	57.5	17.0	747	2	T39879 hypothetical prote
22	57	16.8	327	2	T51571 hypothetical prote
23	57	16.8	617	2	JC5814 LIM motif-containi
24	57	16.8	638	2	JC5813 LIM motif-containi
25	56.5	16.7	906	2	AE2533 hypothetical prote
26	56.5	16.7	520	2	T16593 hypothetical prote
27	56.5	16.7	647	2	G71490 hypothetical prote
28	56.5	16.7	894	2	T20625 ABC transporter, A
29	56	16.5	318	2	H96917

30	56	16.5	381	2	T22008 hypothetical prote
31	56	16.5	595	1	TYCHRL transforming prote
32	56	16.5	942	2	G3861 ARP-dependent DNA
33	55.5	16.4	542	2	S45557 resB protein - Bac
34	55.5	16.4	866	2	C71509 probable DNA polym
35	55.5	16.4	983	2	T19874 hypothetical prote
36	55.5	16.4	1067	2	T39449 probable importin
37	55	16.2	800	2	S29344 protein kinase KIN
38	55	16.2	2555	2	C69681 peptide synthetase
39	54.5	16.1	278	2	H86824 phosphoesterase ho
40	54.5	16.1	309	2	B95078 metallo-beta-lacta
41	54.5	16.1	309	2	G97945 conserved hypothet
42	54.5	16.1	355	2	AC1661 hypothetical prote
43	54.5	16.1	355	2	AE1289 hypothetical prote
44	54.5	16.1	373	2	T10341 late expression fa
45	54.5	16.1	391	2	E69494 2-hydroxyglutaryl-

ALIGNMENTS

RESULT 1
S60226
cytokine IGIF - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence-revision 19-Apr-1996 #text-change 20-Jun-2000
C:Accession: S60226
R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig
Nature 378, 88-91, 1995
A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A:Reference number: S60226; MUID:96061009
A:Accession: S60226
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-192 <OK>
C:Cross-references: EMBL: D49949; NID: g1064822; PDB: BAA08705.1; PDB: g1064823
C:Superfamily: Mus musculus cytokine IGIF

Query Match 55.0%; Score 186.5; DB 2; Length 192;
Best Local Similarity 58.5%; Pred. No. 8.8e-16;
Matches 38; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 2 FGLKLESLKSLVIRNLNDQVLFIIDGNRPLEFMDSDCRNAPRTITFLISMVKDSQPRGMA 61
Db 37 FGLRHTTAVIRNLNDQVLFVDK-RQPFEDMTDIDQSASEPQTRILITYMKDSVEVGIA 95
QY 62 VTLSV 66
Db 96 VTLSV 100

RESULT 2
A28121
major mezozoite surface antigen - Plasmodium yoelii (fragment)
C:Species: Plasmodium yoelii
C:Date: 30-Jun-1989 #sequence-revision 30-Jun-1989 #text-change 26-Aug-1999
R:Burns Jr., J.M.; Daly, T.M.; Vaidya, A.B.; Long, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 602-606, 1988
A:Title: The 3' portion of the gene for a Plasmodium yoelii mezozoite surface antigen
A:Reference number: A28121; MUID:88124889
A:Accession: A28121
A:Molecule type: DNA
A:Residues: 1-680 <BUR>
A:Cross-references: GB: J03612; NID: g160678; PDB: g160679
A:Experimental source: strain 17XL
A:Note: The authors translated the codon GTA for residue 429 as Leu
C:Superfamily: major mezozoite surface antigen
C:Keywords: surface antigen

Query Match 20.6%; Score 70; DB 2; Length 680;

Best Local Similarity 25.7%; Pred. No. 1.5; Mismatches 26; Indels 14; Gaps 3;

Matches 19; Conservative 15; Mismatches 26; Indels 14; Gaps 3;

OY 2 FGKLESLVIRNLN--DOVLFIDGCRPLFE-----DMTSDCRDAPRTIFII 49

Db 159 YSRLELRK--KNINLGERISYVSGLHVFEERKELIKDKDYTGKKNPDNAPEVTNAF 216

OY 50 SMYKDSOPRCMAVT 63

Db 217 EYKELPKGVTVS 230

RESULT 3
major merozoite surface antigen precursor - Plasmodium yoelii

C:Species: Plasmodium yoelii

C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-Aug-1999

C:Accession: A45532; MUID:90014981

A:Title: Cloning and analysis of the gene encoding the 230-kilodalton merozoite surface

A:Reference number: A45532

A:Accession: A45532

A:Molecule type: DNA

A:Residues: 1-1772 <LEW>

A:Cross-references: GB:J04668; NID:g160492; PID:g160493

Mol. Biochem. Parasitol. 36, 283-285, 1989

Mol. Biochem. Parasitol. 36, 283-285, 1989

A:Title: Precursor to the major merozoite surface antigen of Plasmodium yoelii: cloning

A:Reference number: A45531; MUID:90014982

A:Accession: A45531

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 454-1094 <DAL>

A:Cross-references: GB:J03975; NID:g160081; PID:g160082

C:Superfamily: major merozoite surface antigen

C:Keywords: surface antigen

Query Match 20.6%; Score 70; DB 2; Length 1772;

Best Local Similarity 25.7%; Pred. No. 4.5; Mismatches 26; Indels 14; Gaps 3;

Matches 19; Conservative 15; Mismatches 26; Indels 14; Gaps 3;

OY 2 FGKLESLVIRNLN--DOVLFIDGCRPLFE-----DMTSDCRDAPRTIFII 49

Db 1251 YSRLELRK--KNINLGERISYVSGLHVFEERKELIKDKDYTGKKNPDNAPEVTNAF 1308

OY 50 SMYKDSOPRCMAVT 63

Db 1309 EYKELPKGVTVS 1322

RESULT 4
probable hexosyltransferase (EC 2.4.1.-) ag_572 [similarity] - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: D70351

C:Deleerslijder, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.F.; Oy

V.

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666

A:Accession: D70351

A:Molecule type: mRNA

A:Residues: 1-366 <AQF>

A:Cross-references: GB:AE000696; NID:g2983196; PID:NAAC06809.1; PID:g2983210; GB:AE00069

A:Experimental source: strain VF5

C:Superfamily: probable hexosyltransferase ytxN

C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 18.9%; Score 64; DB 1; Length 366;

Best Local Similarity 29.4%; Pred. No. 4; Mismatches 30; Indels 6; Gaps 3;

Matches 20; Conservative 12; Mismatches 30; Indels 6; Gaps 3;

OY 3 GKLESLVIRNLNDOVLFIDGCRPLFEEDMTSDC-----RDNAPTIFILSMYKDSOP 57

Db 130 GVIAKKLVFFGNGFTDVCVFSYQKRLYEEL-DSFCVYIYNGIDPFFVSEKRLNP 168

OY 58 RGMAYTIS 65

Db 189 RNRILTVS 196

RESULT 5
probable RING zinc finger protein, 53384-54880 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: G96835

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

anssen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzita

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: G96835

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-407 <STO>

A:Cross-references: GB:AE005173; NID:96751714; PID:NAF27696.1; GSPDB:GN00141

C:Genetics:

A:Gene: F516.15

A:Map position: 1

Query Match 18.6%; Score 63; DB 2; Length 407;

Best Local Similarity 35.8%; Pred. No. 6; Mismatches 17; Indels 8; Gaps 3;

Matches 19; Conservative 9; Mismatches 17; Indels 8; Gaps 3;

OY 10 SVIRN--LINDO-VLFIDGCRPLFEEDMTSDCGRDAPRTIFILSMYKDSOPRG 59

Db 5 SIVRNTITLQDPLMDHGRNREHIVDITNSDEDDSSR-----SSUDELTPOG 52

RESULT 6
major merozoite surface antigen precursor - Plasmodium chabaudi chabaudi

C:Species: Plasmodium chabaudi chabaudi

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999

C:Accession: A45546

C:Deleerslijder, W.; Hendrix, D.; Bendahman, N.; Haneegrefts, J.; Brils, L.; Hamers-Ca

Mol. Biochem. Parasitol. 43, 231-244, 1990

A:Title: Molecular cloning and sequence analysis of the gene encoding the major meroz

A:Accession: A45546; MUID:91218805

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1785

A:Cross-references: GB:M34947; NID:g160597; PID:g160598

C:Superfamily: major merozoite surface antigen

C:Keywords: surface antigen

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2002, 11:02:44 ; Search time 84.17 seconds
(without alignments)
44,868 Million cell updates/sec

Title: US-09-780-035-71

Perfect score: 173
Sequence: 1 FLACEKERDLFKLLKKEDELGRSIMFTVQNEED 34

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq.032802:*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	173	100.0	34	22	AA65457
2	173	100.0	157	17	AA99564
3	173	100.0	157	17	AA99558
4	173	100.0	157	18	AA15701
5	173	100.0	157	18	AA24258
6	173	100.0	157	19	AAW7158
7	173	100.0	157	19	AAW7207
8	173	100.0	157	19	AAW7080
9	173	100.0	157	19	AAW7083
10	173	100.0	157	19	AAW7084
11	173	100.0	157	19	AAW7088

12	173	100.0	157	19	AAW48961	Mutant human inter
13	173	100.0	157	19	AAW48962	Mutant human inter
14	173	100.0	157	19	AAW48966	Mutant human inter
15	173	100.0	157	19	AAW63810	Human IL-18 protel
16	173	100.0	157	19	AAW37741	IFN-gamma inducing
17	173	100.0	157	19	AAW52176	Interleukin-18 rec
18	173	100.0	157	20	AAV39799	Human interleukin-
19	173	100.0	157	21	AAV44597	Sequence of a matu
20	173	100.0	157	21	AAV53904	Human interleukin-
21	173	100.0	157	21	AAV57570	Human interleukin-
22	173	100.0	157	22	AAE06661	Human interleukin-
23	173	100.0	157	22	AAE82408	Human interleukin-
24	173	100.0	157	22	AAE65294	Human interleukin-
25	173	100.0	157	22	AAE65351	Human interleukin-
26	173	100.0	158	21	AAW85167	Human interleukin-
27	173	100.0	180	19	AAW48959	Human interleukin-
28	173	100.0	181	21	AAW83797	Wild-type human in
29	173	100.0	193	17	AAW9560	Human interleukin
30	173	100.0	193	18	AAW1757	Human interleukon-g
31	173	100.0	193	18	AAW22047	Interferon gamma I
32	173	100.0	193	18	AAW77082	Interferon gamma I
33	173	100.0	193	19	AAW37740	Interleukin 18 act
34	173	100.0	193	19	AAW52172	Interleukin-gamma i
35	173	100.0	193	19	AAW47429	Interleukon-gamma p
36	173	100.0	193	19	AAW46592	Amino acid sequenc
37	173	100.0	193	21	AAW53908	Human IL-18 with
38	173	100.0	193	22	AAW82409	Macaca cynomolgus
39	173	100.0	193	22	AAW30541	A human IL-18
40	173	100.0	193	22	AAW63830	Human interleukin-
41	166	96.0	193	22	AAW72608	Human interleukin
42	163	94.2	157	19	AAW77081	Human interleukin
43	163	94.2	157	19	AAW77085	Human interleukin
44	163	94.2	157	19	AAW77086	Human interleukin
45	163	94.2	157	19	AAW77087	Human interleukin

ALIGNMENTS

RESULT 1	AA65457	standard; protein; 34 AA.
ID	AA65457	
XX	AA65457	
AC	AA65457	
XX	30-NOV-2001	(first entry)
DT	30-NOV-2001	
XX	Human interleukin-18 (IL-18) protein C-terminal fragment.	
DE	Human interleukin-18 (IL-18) protein C-terminal fragment.	
KW	IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;	
KW	neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiant;	
KW	immunosuppressive; antidepressant; neuroleptic; hepatotropic.	
XX		
OS	Homo sapiens.	
XX		
PD	WO200158956-A2.	
PN	16-AUG-2001.	
XX		
PF	09-FEB-2001; 2001WO-US04170.	
PR	10-FEB-2000; 2000US-0181608.	
XX		
PA	(BAD) BASF AG.	
XX		
PI	Ghayur T, Dixon RW, Boguska M, White M, Labkovsky B, Salfield J;	
PI	Duncan AR, Brocklehurst SM, Mankovich J, Shortrock CP, Thompson JE;	
PI	Lennard SN;	
XX		
DR	WPI; 2001-550020/61.	
XX		
PT	Novel antibodies and compounds capable of binding to human	
PT	interleukin-18 useful for treating, e.g., inflammatory disorders,	

PS Claim 1; Page 40; 48pp; English.
 XX A novel human protein (AAR99558) induces interferon-gamma (IFN-gamma)
 CC prodn. by immunocompetent cells. It enhances the cytotoxicity of
 CC killer cells and/or induces the formation of killer cells (e.g.
 CC NK cells, lymphokine-activating killer (LAK) cells, and cytotoxic
 CC T-cells). Recombinant IFN-gamma inducer protein can be produced in
 CC high yields using host cells, esp. Escherichia coli, transformed
 CC with a vector carrying the encoding cDNA (AAR32402). It is useful
 CC as an antiviral, antitumor, antibacterial, immunoregulatory and
 CC blood platelet enhancing agent, and can be used in adoptive
 CC immunotherapy. It is also used to raise monoclonal antibodies.
 CC A full-length sequence is given in AAR99560.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 173; DB 17; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5, 7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FLACEKERDLFKLLIKKEDELGDRSIMFTYONED 34
 Db 124 flacekerdlfklllkedelgdrsimftvqned 157

RESULT 4
 AAW15701 standard; protein: 157 AA.
 XX
 AC AAW15701;
 XX
 DT 26-JAN-1998 (first entry)
 XX
 DE Interferon-gamma inducer protein.
 XX
 KM Interferon-gamma, IFN-gamma; antiviral; antineoplastic; radiotherapy;
 KM immunoregulatory; antitumor agent; chemotherapy; leukopenia;
 KW thrombocytopenia; immunocompetent cell; asthma; hayfever;
 KW rheumatism; interleukin; killer cell.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 73
 FT /label= Ile, Thr
 XX
 PM EP67178-A1.
 XX
 PD 09-APR-1997.
 XX
 PF 26-SEP-1996; 96EP-0306997.
 XX
 PR 20-SEP-1996; 96UP-0269105.
 PR 26-SEP-1995; 95UP-0270725.
 PR 29-FEB-1996; 96JP-0067434.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Arita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T;
 XX
 DR WPI; 1997-205381/19.
 XX
 PT Human protein that induces interferon-gamma prodn. in
 PT immuno:competent cells - useful for adoptive immuno:therapy of
 PT tumours and as antimicrobial agent etc.
 XX
 PS Claim 8; Page 20; 26pp; English.
 XX
 CC The present sequence represents a novel protein from human cells, which
 CC induces interferon-gamma (IFN gamma) production in immunocompetent cells.
 CC This protein enhances cytotoxicity of killer cells and induces their
 CC formation. It is used as an antineoplastic agent for antitumour

CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent,
 CC and in the treatment of atopic or immune system diseases, e.g. asthma,
 CC hayfever or rheumatism. When formulated with interleukin-3, it is also
 CC used to treat leukopenia and thrombocytopenia associated with
 CC radiotherapy or chemotherapy of leukemia and other cancers. When used in
 CC antitumor immunotherapy, this novel protein significantly improves the
 CC immunotherapeutic effect of interleukin-2 (IL-2), compared with use of
 CC IL-2 alone, either when administered to the patient (before
 CC administration of IL-2) or by addition to the medium in which cells
 CC (intended for return to the patient) are being grown.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 173; DB 18; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5, 7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FLACEKERDLFKLLIKKEDELGDRSIMFTYONED 34
 Db 124 flacekerdlfklllkedelgdrsimftvqned 157

RESULT 5
 AAW24258 standard; Protein: 157 AA.
 XX
 AC AAW24258;
 XX
 DT 15-OCT-1997 (first entry)
 XX
 DE Human protein for induction of interferon-gamma.
 XX
 KM Interferon-gamma; immunocompetent cell; malignant tumour;
 KM viral disease; bacterial infection; immune disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 73
 FT /note= "Encoded by AYT"
 XX
 PM JP09157180-A.
 XX
 PD 17-JUN-1997.
 XX
 PF 24-JAN-1996; 96UP-0028722.
 XX
 PR 04-OCT-1995; 95UP-0279906.
 PR 10-MAR-1995; 95JP-0078357.
 PR 29-SEP-1995; 95JP-0274988.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 DR WPI; 1997-369391/34.
 DR N-PSDB; AAT80209.
 XX
 PT A drug containing a polypeptide which induces interferon-gamma -
 PT useful for treating e.g. malignant tumours, viral, bacterial or
 PT immune diseases
 XX
 PS Claim 1; Page 9; 12pp; Japanese.
 XX
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 173; DB 18; Length 157;

Best Local Similarity 100.0%; Pred. No. 5.7e-18;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLACERDLFKLLKKEDELGRSIMPVQNE D 34
124 flacekerdlfkllkkelgdrsimftvqned 157

RESULT 6

AAW77158
ID AAW77158 standard; Peptide; 157 AA.

AC AAW77158;

DT 26-NOV-1998 (first entry)

DE Human Interleukin-18 protein (IL-18).

XX Human; Interleukin-18 receptor; IL-18R; cytokine; signal transduction;

KW immune system; treatment; autoimmune; allergic disease;

KM immunosuppressant.

XX Homo sapiens.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Misc-difference 73 /note="Ile or Thr"

XX EP864585-A1.

PD 16-SEP-1998.

XX 23-DEC-1997; 97EP-0310517.

XX 09-OCT-1997; 97JP-0291837.

XX 12-MAR-1997; 97JP-0074697.

XX 28-JUL-1997; 97JP-0215488.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Kurimoto M, Okura T, Torioge K;

XX WPI; 1998-469188/41.

XX Interleukin-18 receptor polypeptide(s) - and corresponding DNA,

XX which peptide compounds are useful for treating auto-immune or

XX allergic diseases

XX Disclosure: Pages 41-42; 51pp; English.

XX The present sequence represents a human interleukin-18 (IL-18)

XX polypeptide. Interleukin-18 is a type of cytokine which mediates signal

XX transduction in immune systems. The interleukin-18 receptor polypeptide

XX can be used to neutralise interleukin-18 activity or to treat

XX autoimmune or allergic diseases or as an immunosuppressant. Conditions

XX which may be treated include e.g. graft or organ rejection, pernicious

XX anemia, insulin-related diabetes, discoid lupus erythematosus,

XX ulcerative colitis, hyperthyroidism, autoimmune hepatitis, systemic

XX scleroderma, polymyositis, leukopenia, rheumatoid arthritis, HIV

XX infections, asthma, atopic dermatitis, and pollinosis. The products may

XX also be useful in the treatment of septic shock associated with

XX IFN-alpha.

XX Sequence 157 AA;

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Db 124 flacekerdlfkllkkelgdrsimftvqned 157

RESULT 7

AAW77077
ID AAW77077 standard; peptide; 157 AA.

AC AAW77077;

DT 16-NOV-1998 (first entry)

DE Human Interleukin 18.

XX Human; Interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;

KW osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;

KM chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.

XX Homo sapiens.

OS EP861663-A2.

XX 02-SEP-1998.

XX 24-FEB-1998; 98EP-0301352.

XX 25-FEB-1997; 97JP-0055468.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

XX WPI; 1998-448964/39.

XX N-PSDB; AAV48226.

XX Use of Interleukin-18 to inhibit osteoclast formation - in treatment

XX of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,

XX osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,

XX primary hyperthyroidism and osteoporosis

XX Claim 4; Page 18; 56pp; English.

XX Interleukin-18 (IL-18) or a functional equivalent can be used for

XX inhibition of osteoclast formation. IL-18 is used for treating or

XX preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma

XX Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid

XX arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and

XX osteoporosis.

XX Sequence 157 AA;

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XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH misc_difference 38
FT /note= "Cysteine residue replaced with a serine residue"
FT misc_difference 68
FT /note= "Cysteine residue replaced with a serine residue"
FT misc_difference 76
FT /note= "Cysteine residue replaced with an alanine residue"
XX
XX EP861663-A2.
XX
XX 02-SEP-1998.
XX
XX 24-FEB-1998; 98EP-0301352.
XX
XX 25-FEB-1997; 97JP-0055468.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
XX WPI; 1998-448964/39.
XX N-PSDB; AAV48229.
XX
XX Use of interleukin-18 to inhibit osteoclast formation - in treatment
XX of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
XX osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
XX primary hyperthyroidism and osteoporosis
XX
XX Disclosure; Page 22; 56pp; English.
XX
XX Interleukin-18 (IL-18) or a functional equivalent can be used for
XX inhibition of osteoclast formation. IL-18 is used for treating or
XX preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
XX Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
XX arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
XX osteoporosis.
XX
XX Sequence 157 AA:
SQ

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Query Match 100.0%; Score 173; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5.7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKEDELGDRSIMPTVONED 34
 DB 124 flacekerdlfkllkkelgdrsimftvgned 157

```

RESULT 9
AAW77083
ID AAW77083 standard; Peptide; 157 AA.
XX
XX AAW77083;
AC
XX
XX 16-NOV-1998 (first entry)
DT
XX
XX Human interleukin 18 derivative 1.
DE
XX
XX Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
XX osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
XX chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.
OS
XX Homo sapiens.
XX
XX EP861663-A2.
XX
XX 02-SEP-1998.
XX

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PF 24-FEB-1998; 98EP-0301352.
XX
XX 25-FEB-1997; 97JP-0055468.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
XX WPI; 1998-448964/39.
XX
XX Use of interleukin-18 to inhibit osteoclast formation - in treatment
XX of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
XX osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
XX primary hyperthyroidism and osteoporosis
XX
XX Disclosure; Page 30; 56pp; English.
XX
XX Interleukin-18 (IL-18) or a functional equivalent can be used for
XX inhibition of osteoclast formation. IL-18 is used for treating or
XX preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
XX Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
XX arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and
XX osteoporosis.
XX
XX Sequence 157 AA:
SQ

```

Query Match 100.0%; Score 173; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5.7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKEDELGDRSIMPTVONED 34
 DB 124 flacekerdlfkllkkelgdrsimftvgned 157

```

RESULT 10
AAW77084
ID AAW77084 standard; Peptide; 157 AA.
XX
XX AAW77084;
AC
XX
XX 16-NOV-1998 (first entry)
DT
XX
XX Human interleukin 18 derivative 2.
DE
XX
XX Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
XX osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
XX chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.
OS
XX Homo sapiens.
XX
XX EP861663-A2.
XX
XX 02-SEP-1998.
XX
XX 24-FEB-1998; 98EP-0301352.
XX
XX 25-FEB-1997; 97JP-0055468.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;
XX WPI; 1998-448964/39.
XX
XX Use of interleukin-18 to inhibit osteoclast formation - in treatment
XX of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
XX osteosarcoma, chronic rheumatoid arthritis, deformity ostitis,
XX primary hyperthyroidism and osteoporosis
XX
XX Disclosure; Page 30-31; 56pp; English.
XX

```

CC Interleukin-18 (IL-18) or a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 XX
 SQ Sequence 157 AA:

Query Match 100.0%; Score 173; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5.7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKEDELGDRSIMFTVQNEQ 34
 DB 124 flacekerdlfkllkkelgdrsimftvqned 157

RESULT 11

AAW77088 standard; Peptide; 157 AA.

AAW77088;

16-NOV-1998 (first entry)

Human interleukin 18 derivative 6.

Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;
 chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism.

Homo sapiens.

EP861663-A2.

02-SEP-1998.

24-FEB-1998; 98EP-0301352.

25-FEB-1997; 97JP-0055468.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Gillespie MT, Horwood NJ, Kurimoto M, Udagawa N;

WPI; 1998-448964/39.

Use of interleukin-18 to inhibit osteoclast formation - in treatment
 of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 osteosarcoma, chronic rheumatoid arthritis, deformity osteitis,
 primary hyperthyroidism and osteoporosis

Disclosure; Page 33; 56pp; English.

Interleukin-18 (IL-18) or a functional equivalent can be used for
 inhibition of osteoclast formation. IL-18 is used for treating or
 preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid
 arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 osteoporosis.

Sequence 157 AA:

Query Match 100.0%; Score 173; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5.7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKEDELGDRSIMFTVQNEQ 34
 DB 124 flacekerdlfkllkkelgdrsimftvqned 157

RESULT 12

AAW48961 standard; Peptide; 157 AA.

AAW48961;

25-SEP-1998 (first entry)

Mutant human interferon-gamma inducing factor IGIF/MT12.

Interferon-gamma inducing factor; interferon-gamma; killer cell;
 antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
 hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 osteoporosis; thrombopenia; acquired immunodeficiency syndrome.

Homo sapiens.

Synthetic.

EP845530-A2.

03-JUN-1998.

28-NOV-1997; 97EP-0309632.

14-NOV-1997; 97JP-0329715.

29-NOV-1996; 96JP-0333037.

21-JAN-1997; 97JP-0020906.

(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

Kurimoto M, Okamoto I, Yamamoto K;

WPI; 1998-288747/26.

N-PSDB; AAV32625.

Mutants of interferon-gamma inducing polypeptide - useful as
 antitumour, antiviral, antimicrobial or anti-immunopathic agents

Claim 5; page 41; 59pp; English.

The present sequence represents the mutant human interferon-gamma
 inducing factor IGIF/MT12. The wild-type human interferon-gamma
 factor sequence is shown in AAW48959. The invention provides for mutant
 human and mouse interferon-gamma inducing factors (IGIF) in which one
 or more cysteine residues are replaced with different residues at or
 away from the consensus sequences shown in AAW48956-W48958. The mutant
 IGIFs are capable of stimulating immunocompetent cells for the production
 of interferon-gamma and are claimed to be less toxic, more active and
 stable than the corresponding wild type interferon-gamma inducing
 factor. The mutant IGIFs are also claimed to enhance killer cell
 cytotoxicity and/or induce killer cell formation, and may therefore
 be useful as antitumour agents, antitumour immunotherapeutics, antiviral
 agents and antimicrobial agents. The mutant IGIFs are also claimed
 to be useful for treating hepatitis, acquired immunodeficiency syndrome
 (AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal
 carcinoma), rheumatism, osteoporosis and thrombopenia caused by
 radiation- and chemo-therapy.

Sequence 157 AA:

Query Match 100.0%; Score 173; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5.7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKEDELGDRSIMFTVQNEQ 34

Db 124 flacekerdflklllkedlgsrsmftvqned 157

RESULT 13

AAW48962 ID AAW48962 standard; Peptide: 157 AA.

AC AAW48962;

DT 25-SEP-1998 (first entry)

DE Mutant human interferon-gamma inducing factor IGIF/MUT21.

XX Interferon-gamma inducing factor; interferon-gamma; killer cell;
 KW antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
 KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
 XX Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Misc-difference 38 /note="changed from Cys in wild-type to Ser in
 mutant"

PN EP845530-A2.

PD 03-JUN-1998.

PF 28-NOV-1997; 97EP-0309632.

PR 14-NOV-1997; 97JP-0329715.

PR 29-NOV-1996; 96JP-0333037.

PR 21-JAN-1997; 97JP-0020906.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Kurimoto M, Okamoto I, Yamamoto K;

DR N-PSDB; AAV32626.

PT Mutants of interferon-gamma inducing polypeptide - useful as
 antitumour, antiviral, antimicrobial or anti-immunopathic agents
 Claim 5; page 41; 59pp; English.

XX The present sequence represents the mutant human interferon-gamma
 CC inducing factor IGIF/MUT21. The wild-type human interferon-gamma
 CC factor sequence is shown in AAW48959. The invention provides for mutant
 CC human and mouse interferon-gamma inducing factors (IGIF) in which one or
 CC more cysteine residues are replaced with different residues at or away
 CC from the consensus sequences shown in AAW48956-W48958. The mutant IGIFs
 CC are capable of stimulating immunocompetent cells for the production of
 CC interferon-gamma and are claimed to be less toxic, more active and
 CC stable than the corresponding wild type interferon-gamma inducing
 CC factor. The mutant IGIFs are also claimed to enhance killer cell
 CC cytotoxicity and/or induce killer cell formation, and may therefore
 CC be useful as antitumour agents, antitumour immunotherapeutics, antiviral
 CC agents and antimicrobial agents. The mutant IGIFs are also claimed
 CC (AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal
 CC carcinoma), rheumatism, osteoporosis and thrombopenia caused by
 CC radiation- and chemo-therapy.

SO Sequence 157 AA;

Query Match 100.0%; Score 173; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5.7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLACEKERDLPKLLKKEDELGDRSMFTVQNEED 34
 Db 124 flacekerdflklllkedlgsrsmftvqned 157

RESULT 14

AAW48966 ID AAW48966 standard; Peptide: 157 AA.

AC AAW48966;

DT 25-SEP-1998 (first entry)

DE Mutant human interferon-gamma inducing factor IGIF/MUT35.

XX Interferon-gamma inducing factor; interferon-gamma; killer cell;
 KW antitumour agent; antiviral agent; antimicrobial agent; tumour; IGIF;
 KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;
 KW osteoporosis; thrombopenia; acquired immunodeficiency syndrome.
 XX Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Misc-difference 38 /note="changed from Cys in wild-type to Ser in
 mutant"

PN EP845530-A2.

PD 03-JUN-1998.

PF 28-NOV-1997; 97EP-0309632.

PR 14-NOV-1997; 97JP-0329715.

PR 29-NOV-1996; 96JP-0333037.

PR 21-JAN-1997; 97JP-0020906.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Kurimoto M, Okamoto I, Yamamoto K;

DR N-PSDB; AAV32630.

PT Mutants of interferon-gamma inducing polypeptide - useful as
 antitumour, antiviral, antimicrobial or anti-immunopathic agents
 Claim 5; page 43; 59pp; English.

XX The present sequence represents the mutant human interferon-gamma
 CC inducing factor IGIF/MUT35. The wild-type human interferon-gamma
 CC factor (IGIF) sequence is shown in AAW48959. The invention provides for
 CC mutant human and mouse interferon-gamma inducing factors in which one
 CC or more cysteine residues are replaced with different residues at or
 CC away from the consensus sequences shown in AAW48956-W48958. The mutant
 CC IGIFs are capable of stimulating immunocompetent cells for the production
 CC of interferon-gamma and are claimed to be less toxic, more active and
 CC stable than the corresponding wild type IGIF. The mutant IGIFs are also
 CC claimed to enhance killer cell cytotoxicity and/or induce killer cell
 CC formation, and may therefore be useful as antitumour agents, antitumour
 CC immunotherapeutics, antiviral agents and antimicrobial agents. The
 CC mutant IGIFs are also claimed to be useful for treating hepatitis,
 CC acquired immunodeficiency syndrome (AIDS), malaria, tuberculosis, solid
 CC malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
 CC thrombopenia caused by radiation- and chemo-therapy.

SO Sequence 157 AA;

Query Match 100.0%; Score 173; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5,7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKDELDGDRSIMFTYQNE D 34
 Db 124 flacekerdlfkllkkedelgdrsimftvqned 157

RESULT 15

AAW63810
 ID AAW63810 standard; protein; 157 AA.

XX AAW63810;

XX 28-SEP-1998 (first entry)

XX Human IL-18 protein fragment.

XX Interleukin-18: IL-18; human; treatment; autoimmune disease; antibody;

XX immunosuppressant; inhibitor; receptor protein; detection.

XX Homo sapiens.

XX key Location/Qualifiers

XX Protein 1..157

XX /label= IL-18

XX /note= "partial sequence"

XX Misc-difference 73

XX /label= Thr or Ile

XX EP850952-A1.

XX 01-JUL-1998.

XX 23-DEC-1997; 97EP-0310555.

XX 28-JUL-1997; 97JP-0215490.

XX 26-DEC-1996; 96JP-0356426.

XX 21-FEB-1997; 97JP-0052526.

XX 06-JUN-1997; 97JP-0163490.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Kunikata T, Kurimoto M, Torigoe K, Ushio S;

XX WPI: 1998-335317/30.

XX New interleukin-18 receptor protein used to inhibit interleukin-18,

XX to treat autoimmune disease and as immunosuppressant - and new

XX monoclonal antibody and hybridoma used to detect interleukin-18

XX receptor protein

XX Claim 5; Page 16; 35pp; English.

XX This sequence represents a human interleukin-18 (IL-18) fragment which is

XX used in a method involved in neutralising IL-18 or to treat autoimmune

XX diseases or as an immunosuppressant using anti-IL-18 antibodies which

XX can inhibit IL-18. Such antibodies can also be used to detect the IL-18

XX receptor protein (labelled with an enzyme or a radioactive or fluorescent

XX substance). The protein is used to treat e.g. graft rejection, pernicious

XX anaemia, atrophic gastritis, insulin-resistant diabetes, Wegener

XX granulomatosis, discoid lupus erythematosus, ulcerative colitis,

XX cold-agglutinin-related diseases, Goodpasture's syndrome, primary

XX biliary cirrhosis, Sjogren syndrome, autoimmune hepatitis, autoimmune

XX onset type diabetes, Sjogren syndrome, autoimmune hepatitis, autoimmune

XX haemolytic anaemia, myasthenia gravis, systemic scleroderma, systemic

XX lupus erythematosus, polyepilectic cold haemaglobinuria, polymyositis,

XX periarthritis nodosa, multiple sclerosis, Addison's disease, purpura

XX haemorrhagica, Basedow's disease, leukopenia, Behcet's disease,

XX climacterium praecox, rheumatoid arthritis, rheumatopyra, chronic

XX thyroiditis, Hodgkin's disease, HIV, asthma, atopic dermatitis, allergic

CC naititis, pollinosis, aptioxin-allergy and septic shock resulting from
 CC production or administration of excessive gamma interferon (IFN-gamma).
 XX
 SQ Sequence 157 AA;

Query Match 100.0%; Score 173; DB 19; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5,7e-18;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKDELDGDRSIMFTYQNE D 34
 Db 124 flacekerdlfkllkkedelgdrsimftvqned 157

Search completed: October 9, 2002, 11:02:44
 Job time: 6455 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 11:04:48 ; Search time 56.97 Seconds
(Without alignments)
57.347 Million cell updates/sec

Title: US-09-780-035-71

Perfect score: 173

Sequence: 1 FLACEKERDLFKLLKKEDELGDRSIMFTVQNE 34

Scoring table: BLOSUM62

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR-71:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Listing first 45 summaries

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	123	71.1	192	2	cytokine IGIF - mo
2	58	33.5	499	2	monomine oxidase
3	53.5	30.9	1359	2	hypothetical prote
4	53	30.6	259	1	site-specific DNA-
5	53	30.6	730	2	fasciclin IV precu
6	52.5	30.3	356	2	hypothetical prote
7	52	30.1	217	2	two component resp
8	52	30.1	262	2	hypothetical prote
9	52	30.1	1277	2	hypothetical prote
10	51.5	29.8	429	2	hypothetical prote
11	51.5	29.8	432	2	enolase [imported]
12	51.5	29.8	1119	2	phosphopyruvate hy
13	51.5	29.8	2262	2	nuclear matrix con
14	51.5	29.5	307	2	large protein L -
15	51	29.5	307	4	catechol 2,3-dioxy
16	51	29.5	339	2	catechol 2,3-dioxy
17	51	29.5	354	2	hypothetical prote
18	51	29.5	357	2	response regulator
19	51	29.5	431	2	hypothetical prote
20	50.5	29.2	384	2	conserved hypotet
21	50	28.9	195	2	probable N-acetyl
22	50	28.9	258	2	hypothetical prote
23	50	28.9	258	2	flagellar export p
24	50	28.9	314	2	probable flagellar
25	50	28.9	643	2	catechol 2,3-dioxy
26	50	28.9	3944	2	probable transcrip
27	49.5	28.6	231	2	hypothetical prote
28	49	28.3	94	1	DNA repair/recomb
29	49	28.3	186	2	S-100 protein alph
					hypothetical prote

30	49	28.3	307	2	JC2503	catechol 2,3-dioxy
31	49	28.3	307	2	JC4885	catechol 2,3-dioxy
32	49	28.3	399	2	E84964	hypothetical prote
33	49	28.3	407	2	AE1073	phosphopentomutase
34	49	28.3	420	2	T02363	hypothetical prote
35	49	28.3	440	2	F70117	hypothetical prote
36	49	28.3	1195	2	S38174	probable purine nu
37	49	28.3	1459	2	S50437	hypothetical prote
38	48.5	28.0	124	2	A64391	hypothetical prote
39	48.5	28.0	475	1	A56824	diolipomamide d
40	48.5	28.0	1004	2	H81683	helicase, probable
41	48.5	28.0	1036	2	E96682	hypothetical prote
42	48	27.7	146	2	T16561	hypothetical prote
43	48	27.7	150	2	S01770	Spec2a protein - s
44	48	27.7	190	2	J01790	Salp15R protein -
45	48	27.7	238	2	C82884	conserved hypotet

ALIGNMENTS

RESULT 1
S60226
cytokine IGIF - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: S60226
R:Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torig
Nature 378, 88-91, 1995
A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A:Reference number: S60226; MUID:96061009
A:Accession: S60226
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-192 <OKA>
A:Cross-references: EMBL:D49949; NID:g1064822; PIDN:BAA08705.1; PID:g1064823
C:Superfamily: Mus musculus cytokine IGIF

Query Match 71.1%; Score 123; DB 2; Length 192;
Best Local Similarity 71.9%; Pred. No. 1.8e-09;
Matches 23; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKEDELGDRSIMFTVQNE 32
DB 157 FLACQKEDDAFLKLLKKEDELGDRSVMTVLTN 188

RESULT 2

151346
monomine oxidase - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: 151346

R:Chen, K.; Wu, H.F.; Grimsby, J.; Shih, J.C.
Mol. Pharmacol. 46, 1226-1233, 1994

A:Title: Cloning of a novel monomine oxidase cDNA from trout liver.

A:Reference number: 151346; MUID:95107295

A:Accession: 151346

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-499 <CHE>

A:Cross-references: GB:L37878; NID:g728484; PIDN:AAA64302.1; PID:g728485

A:Gene: MAO

Query Match 33.5%; Score 58; DB 2; Length 499;
Best Local Similarity 46.4%; Pred. No. 4.2;
Matches 13; Conservative 6; Mismatches 7; Indels 2; Gaps 1;

QY 6 KERDLFKLLKKEDELGDRSIMFTVQNE 33

Db 26 KEGSLPVLLEARDRVGRT--FTVQNE 51

RESULT 3

T34036
 Hypothetical protein B0041.7 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T34036
 R:Fulton, R.; Wohldmann, P.
 Submitted to the EMBL Data Library, April 1997
 A:Description: The sequence of *C. elegans* cosmid B0041.
 A:Reference number: 221466
 A:Accession: T34036
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1359 <FUL>
 A:Cross-references: EMBL:AF000196; PIDN:AAC24256.1; GSPDB:GN00019; CESP:B0041.7
 A:Experimental source: strain Bristol N2; clone B0041
 C:Genetics:
 A:Gene: CESP:B0041.7
 A:Map position: 1
 A:Introns: 12/2; 59/2; 248/2; 582/1; 675/1; 733/3; 966/2; 1044/2; 1310/3

Query Match

Best Local Similarity 35.1%; Score 53.5; DB 2; Length 1359;
 Matches 13; Conservative 9; Mismatches 6; Indels 9; Gaps 1;

OY 2 LACEKERDLFKL-----TLKKEDELGDRSIMFTV 29

Db 934 LVKEERDDFALSKRLILVELIKKECEIGDKLWFS 970

RESULT 4

site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) - phage T2
 C:Species: phage T2
 C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 05-May-2000
 C:Accession: A30195
 R:Miner, Z.; Hattman, S.
 J. Bacteriol. 170, 5177-5184, 1988
 A:Title: Molecular cloning, sequencing, and mapping of the bacteriophage T2 dam gene.
 A:Reference number: A30195; MUID:89033901
 A:Accession: A30195
 A:Molecule type: DNA
 A:Residues: 1-259 <MIN>
 A:Cross-references: GB:M22342; NID:g215792; PIDN:AAA32477.1; PID:g215793
 A:Gene: dam
 C:Genetics:
 A:Superfamily: site-specific methyltransferase (adenine-specific) EcoRV
 C:Keywords: methyltransferase; S-adenosylmethionine

Query Match

Best Local Similarity 40.6%; Score 53; DB 1; Length 259;
 Matches 13; Conservative 5; Mismatches 10; Indels 4; Gaps 1;

OY 1 FLACEKERDLFKLILKKEDELGDRSIMFTVON 32

Db 184 FWSEBEKDLNML-----DSLMDRGITKRLSN 211

RESULT 5

JH0798
 Fasciclin IV precursor - American bird grasshopper
 C:Species: *Schistocerca americana* (American bird grasshopper)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: JH0798
 R:Kolodkin, A.; Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Good
 Neuron 9, 831-845, 1992
 A:Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance in

A:Reference number: JH0798; MUID:93040225

A:Accession: JH0798

A:Molecule type: mRNA

A:Residues: 1-730 <KOI>

A:Cross-references: GB:L00709; NID:g160844; PID:g160845

A:Experimental source: embryo

C:Comment: This protein plays a role in growth cone guidance in the developing centra

C:Keywords: glycoprotein; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-730/Product: fasciclin IV #status predicted <MAT>

F:23-627/Domain: extracellular #status predicted <EXT>

F:628-652/Domain: transmembrane #status predicted <TM>

F:653-730/Domain: intracellular #status predicted <INT>

F:44,71,163,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 36.1%; Score 53; DB 2; Length 730;
 Matches 13; Conservative 7; Mismatches 14; Indels 2; Gaps 1;

OY 1 FLACEKERDLFKLILKKEDEL--GDRSIMFTVONED 34

Db 41 FLGNESHKHDFKLEKDHNSLWGANRIVYNISLRD 76

RESULT 6

S55181
 Hypothetical protein YJL131C - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein J0682

C:Species: *Saccharomyces cerevisiae*

C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 29-Oct-1999

C:Accession: S55181; S05768; S56913; S71666; PQ0003

R:Katsoulou, C.; Tzermia, M.; Alexandraki, D.

Submitted to the EMBL Data Library, May 1995

A:Description: The complete sequence of a 40.7 kb segment located on the left arm of

yeast hypothetical proteins.

A:Reference number: S55159

A:Accession: S55181

A:Molecule type: DNA

A:Residues: 1-356 <KAT>

A:Cross-references: EMBL:X87371; NID:g854542; PIDN:CAA60824.1; PID:g854565

R:Souciety, J.L.; Nagy, M.; le Gouar, M.; Lacroute, F.; Potier, S.

Gene 79, 59-70, 1989

A:Title: Organization of the yeast URA2 gene: identification of a defective dihydrot

A:Reference number: S05766; MUID:89378778

A:Accession: S05768

A:Molecule type: DNA

A:Residues: 1-124 <SOU>

A:Cross-references: EMBL:M27174

R:Katsoulou, C.; Tzermia, M.; Alexandraki, D.

Submitted to the Protein Sequence Database, September 1995

A:Reference number: S56912

A:Accession: S56913

A:Molecule type: DNA

A:Residues: 1-356 <KAW>

A:Cross-references: EMBL:249406; NID:g1008333; PIDN:CAA89426.1; PID:g1008334; MIPS:YJ

R:Katsoulou, C.; Tzermia, M.; Tavernarakis, N.; Alexandraki, D.

Yeast 12, 787-797, 1996

A:Title: Sequence analysis of a 40.7 kb segment from the left arm of yeast chromosome

of chromosome XI.

A:Reference number: S71666

A:Accession: S71666

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-356 <KAF>

A:Cross-references: EMBL:X87371; NID:g854542; PIDN:CAA60824.1; PID:g854565

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995

C:Genetics:

A:Map position: 10L

Query Match

Best Local Similarity 33.3%; Score 52.5; DB 2; Length 356;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 11:15:54 ; Search time 40.26 Seconds
(without alignments)
32.699 Million cell updates/sec

Title: US-09-780-035-71

Perfect score: 173
Sequence: 1 FLACERKDLPLKLEDELGRSIMPVONED 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	173	100.0	193	IL18_HUMAN	Q14116 homo sapien
2	141	81.5	193	IL18_HORSE	O9XSG7 equus cabal
3	139	80.3	192	IL18_PIG	O19073 sus scrofa
4	134	77.5	193	IL18_CANFA	O9XSR0 canis fam11
5	131	75.7	193	IL18_BOVIN	O9TU73 bos taurus
6	123	71.1	192	IL18_MOUSE	P70380 mus musculu
7	119	68.8	194	IL18_RAT	P97336 rattus norv
8	58	33.5	522	IL18_RAT	P49253 rattus norv
9	53.5	30.9	1359	ATRX_CAEEL	O9U7E0 caenorhabdi
10	53	30.6	259	DMA_BPT2	P12427 bacterioph
11	53	30.6	730	SMIA_SCHAM	Q26473 schistocerc
12	52.5	30.3	101	S107_BOVIN	Q28050 bos taurus
13	52.5	30.3	356	YJN1_YEAST	P47015 saccharomy
14	52	30.1	1277	YMW6_YEAST	O04264 saccharomy
15	51.5	29.8	432	ENO_SYNY3	P77972 synechocyst
16	51.5	29.8	2262	RRLP_PL2HT	P26676 human para
17	51	29.5	307	XYEL_PSEPU	P06622 pseudomonas
18	49.5	28.6	231	RECO_COXBU	P51838 coxiella bu
19	49	28.3	93	S10A_BOVIN	P02639 bos taurus
20	49	28.3	93	S10A_RAT	P35467 rattus norv
21	49	28.3	307	XYLE_PSEAR	P27887 pseudomonas
22	49	28.3	399	LOLC_BOVAL	P37382 buchnera ap
23	49	28.3	1195	YK76_YEAST	P36168 saccharomy
24	49	28.3	1459	GEA2_YEAST	P36993 saccharomy
25	48.5	28.0	124	Y729_METUA	O58139 methanococ
26	48.5	28.0	474	DLDH_HAIYO	O04829 halobacteri
27	48	27.7	93	S10A_MOUSE	P55565 mus musculu
28	48	27.7	150	SP2A_STRPU	P04110 strongyloce
29	48	27.7	190	VA52_VACCV	Q01220 vaccinia vi
30	48	27.7	307	NAHI_PSEPU	P08127 pseudomonas
31	48	27.7	326	RNHL_SCHPO	O10236 schizosacch
32	48	27.7	468	FIIB_BOVIN	P02676 bos taurus
33	48	27.7	546	SYR_THEMA	O9X088 thermotoga

34	48	27.7	632	1	PABP_DROME	P21187 drosophila
35	47.5	27.5	400	1	INPP_BOVIN	P21327 bos taurus
36	47	27.2	75	1	DMS2_PACDA	O93452 pachymedusa
37	47	27.2	93	1	S10A_HUMAN	P23297 homo sapien
38	47	27.2	259	1	DMA_BPT4	P04392 bacterioph
39	47	27.2	336	1	SIFA_SALTY	O56061 salmoneella
40	47	27.2	527	1	AOFA_CANFA	P56027 canis fam11
41	47	27.2	4385	1	VP73_CAEEL	O09222 caenorhabdi
42	46.5	26.9	347	1	Y806_METUA	O58212 methanococ
43	46.5	26.9	399	1	INPP_HUMAN	P49441 homo sapien
44	46.5	26.9	434	1	INPP_HUMAN	O02654 loligo peal
45	46.5	26.9	759	1	TRP1_RABIT	O9TUN9 oryctolagus

ALIGNMENTS

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RESULT 1
ID IL18_HUMAN STANDARD: PRT: 193 AA.
AC 014116: 075599;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interleukin-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Liver;
RA MEDLINE=96247646; PubMed=8666798;
RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
RT in Escherichia coli, and studies on the biologic activities of the
RT protein."
RL J. Immunol. 156:4274-4279(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Yong D., Guixin D., Linhua H., Haitao W.;
RT "Cloning and sequencing of the cDNA for precursor hIL-18."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of human Interleukin 18 cDNA."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 2-193 FROM N.A.
RA Conti B., Kim S.-J., Tinti C., Chun H.-S., Joh T.H.;
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN - FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CELLS.
RN - SUBCELLULAR LOCATION: Secreted.
RN - SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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EMBL: D49950; BAA08706.1; -
EMBL: AF077611; AAC27787.1; -

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DR EMBL: AY044641; AAK95950.1; -
 DR EMBL: U90434; AAB50010.1; -
 DR MIM: 600953; -
 DR InterPro: IPR000975; Interleukin_1.
 DR SMART: SM00125; IL1; 1.
 KW Cytokine.
 FT PROPEP 1 36 BY SIMILARITY.
 FT CHAIN 37 193 INTERLEUKIN-18.
 FT CONFLICT 66 66 F -> L (IN REF. 2).
 FT CONFLICT 86 86 S -> R (IN REF. 2).
 FT CONFLICT 191 191 N -> S (IN REF. 2).
 SO SEQUENCE 193 AA; 22326 MW; 323C62C20378BD5 CRC64;

Query Match 100.0%; Score 173; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 1.3e-15;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FLACKEKRDLFKLTKKEDELDGDSIMFTYONED 34
 Db 160 FLACKEKRDLFKLTKKEDELDGDSIMFTYONED 193

RESULT 2
 ID IL18_HORSE STANDARD; PRT; 193 AA.
 AC Q9XS07;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 IL18 OR IGIF.
 OS Equus caballus (Horse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nicolas L., Penha-Goncaves M.N., Keanle J.L., Logan N.A.,
 RA Argyle D.J., Onions D.E.;
 RT "Nucleotide sequence of equine Interleukin 12 and 18 cDNAs";
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CELLS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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 CC -----
 DR EMBL: Y11131; CAA72013.1; -
 KW Cytokine.
 FT PROPEP 1 36 BY SIMILARITY.
 FT CHAIN 37 193 INTERLEUKIN-18.
 SO SEQUENCE 193 AA; 22058 MW; 4DB1535E904ECAP CRC64;

Query Match 81.5%; Score 141; DB 1; Length 193;
 Best Local Similarity 76.5%; Pred. No. 1.8e-11;
 Matches 26; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Oy 1 FLACKEKRDLFKLTKKEDELDGDSIMFTYONED 34
 Db 160 FLACKEKRDLFKLTKKEDELDGDSIMFTYONED 193

RESULT 3
 ID IL18_PIG STANDARD; PRT; 192 AA.
 AC O19073;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
 DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
 IL18 OR IGIF.
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Foss D.L., Murlaugh M.P.;
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Muneta Y., Mori Y.;
 RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=20260994; PubMed=10803849;
 RA Fournout S., Dozois C.M., Verle M., Pinton P., Fairbrother J.M.,
 RA Oswald E., Oswald I.P.;
 RT "Cloning, chromosomal location, and tissue expression of the gene for
 RT pig interleukin-18";
 RL Immunogenetics 51:358-365(2000).
 CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
 AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
 CELLS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
 CC -----
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 CC -----
 DR EMBL: U68701; AAC18415.1; -
 DR EMBL: AB010003; BAA24135.1; -
 DR EMBL: AF191088; AAF71200.1; -
 DR InterPro: IPR000975; Interleukin_1.
 DR SMART: SM00125; IL1; 1.
 KW Cytokine.
 FT PROPEP 1 35 BY SIMILARITY.
 FT CHAIN 36 192 INTERLEUKIN-18.
 SO SEQUENCE 192 AA; 22026 MW; 8B1EA654E221A17A CRC64;

Query Match 80.3%; Score 139; DB 1; Length 192;
 Best Local Similarity 76.5%; Pred. No. 3.3e-11;
 Matches 26; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Oy 1 FLACKEKRDLFKLTKKEDELDGDSIMFTYONED 34
 Db 159 FLACKEKRDLFKLTKKEDELDGDSIMFTYONED 192

RESULT 4
 ID IL18_CANFA STANDARD; PRT; 193 AA.
 AC Q9XS07;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2002, 11:15:01 ; Search time 105.02 Seconds
(without alignments)
56.007 Million cell updates/sec

Title: US-09-780-035-71

Sequence: 1 FLACEKERDLFLIKKEDLGDRSIMFTYQND 34

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

562222

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_RVIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	97.7	193	4	096KJ8
2	166	96.0	193	6	09BGT5
3	147	85.0	192	6	09BGT5
4	131	75.7	178	6	09BGT5
5	128	74.0	192	6	09BGT5
6	128	74.0	193	6	09BGT5
7	108	62.4	196	11	09BGT5
8	65.5	37.9	198	13	09BGT5
9	62	35.8	211	13	09BGT5
10	59	34.1	314	2	09BGT5
11	55.5	32.1	1055	4	09BGT5
12	52.5	30.3	270	11	09BGT5
13	52.5	30.3	391	2	09BGT5
14	52.5	30.3	506	11	09BGT5
15	52	30.1	590	16	09BGT5
16	51.5	29.8	1119	10	004390

17	51.5	29.8	1689	12	09BGT5	09BGT5 crimean-con
18	51.5	29.8	1689	12	09BGT5	09BGT5 crimean-con
19	51.5	29.8	1689	12	09BGT5	09BGT5 crimean-con
20	51	29.5	307	2	09BGT5	09BGT5 crimean-con
21	51	29.5	307	2	09BGT5	09BGT5 crimean-con
22	51	29.5	307	2	09BGT5	09BGT5 crimean-con
23	51	29.5	307	2	09BGT5	09BGT5 crimean-con
24	51	29.5	307	2	09BGT5	09BGT5 crimean-con
25	51	29.5	307	2	09BGT5	09BGT5 crimean-con
26	51	29.5	307	2	09BGT5	09BGT5 crimean-con
27	51	29.5	307	2	09BGT5	09BGT5 crimean-con
28	50.5	29.2	384	16	09BGT5	09BGT5 crimean-con
29	50.5	29.2	384	16	09BGT5	09BGT5 crimean-con
30	50.5	29.2	384	16	09BGT5	09BGT5 crimean-con
31	50	28.9	195	16	051524	051524 botrellia bu
32	50	28.9	258	16	025120	025120 helicobacte
33	50	28.9	258	16	09BGT5	09BGT5 crimean-con
34	50	28.9	258	16	09BGT5	09BGT5 crimean-con
35	50	28.9	258	16	09BGT5	09BGT5 crimean-con
36	50	28.9	258	16	09BGT5	09BGT5 crimean-con
37	50	28.9	258	16	09BGT5	09BGT5 crimean-con
38	50	28.9	258	16	09BGT5	09BGT5 crimean-con
39	50	28.9	258	16	09BGT5	09BGT5 crimean-con
40	49.5	28.6	196	2	09BGT5	09BGT5 crimean-con
41	49.5	28.6	208	3	09BGT5	09BGT5 crimean-con
42	49.5	28.6	208	3	09BGT5	09BGT5 crimean-con
43	49.5	28.6	208	3	09BGT5	09BGT5 crimean-con
44	49.5	28.6	208	3	09BGT5	09BGT5 crimean-con
45	49	28.3	158	2	09BGT5	09BGT5 crimean-con

ALIGNMENTS

RESULT 1
ID 096KJ8 PRELIMINARY: PRT: 193 AA.
AC 096KJ8:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN 18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying P., Jianxin L.
RT "Cloning of Mutant Human Interleukin 18 cDNA."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF380360; AAK57024.1;
SQ SEQUENCE 193 AA: 22323 MW: 265002050187557 CRC64;

Query Match 97.7%, Score 169, DB 4; Length 193;
Best Local Similarity 97.1%, Pred. No. 1,4e-15;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 FLACEKERDLFLIKKEDLGDRSIMFTYQND 34
DB 160 FLACEKERDLFLIKKEDLGDRSIMFTYQND 193
RESULT 2
ID 09BGT5 PRELIMINARY: PRT: 193 AA.
AC 09BGT5:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INTERLEUKIN-18.
GN IL18.

OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9544;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=21229850; PubMed=11331040;
 RA Clivedoni L.D., Imhoof J.D., Parodi L.M., Velasquillo C.M.,
 Hodara V.L.,
 "Expression of the Interleukin-18 gene from Rhesus Macaque by the
 RT Simian Immunodeficiency Virus Does Not Result in Increased Viral
 RT Replication."
 RL J. Interferon Cytokine Res. 21:173-180(2001).
 DR EMBL: AF030732; AAK13416.1;
 SQ SEQUENCE 193 AA; 22325 MW; B2BD29C033BB0B5E CRC64;

Query Match 96.0%; Score 166; DB 6; Length 193;
 Best Local Similarity 94.1%; Pred. No. 3.6e-15;
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKDELDGDSIMFTVQND 34
 DB 160 FLACEKERDLFKLLKKDELDGDSIMFTVQND 193

RESULT 3
 ID 095M33 PRELIMINARY; PRT; 192 AA.
 AC 095M33;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE INTERFERON-GAMMA INDUCING FACTOR.
 GN IGIF.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hanlon L., McGillivray C.P., Argyle D.J.A., Nicolson L., Onions D.E.;
 RT "Nucleotide sequence of feline IGIF cDNA (provisional).";
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y13923; CAC42918.1;
 SQ SEQUENCE 192 AA; 22068 MW; 5878C3DAC7A43358 CRC64;

Query Match 85.0%; Score 147; DB 6; Length 192;
 Best Local Similarity 82.4%; Pred. No. 1.5e-12;
 Matches 28; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKDELDGDSIMFTVQND 34
 DB 159 FLACEKERDLFKLLKKDELDGDSIMFTVQNK 192

RESULT 4
 ID 09M218 PRELIMINARY; PRT; 178 AA.
 AC 09M218;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE INTERLEUKIN-18 (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY, LIVER, BLOOD MONONUCLEAR CELLS;
 RA Olsen S.C., Lee I.K., Wang S.M., Kehrl M., Bolin C.A.;
 RT "Cloning of bovine Interleukin-18, expression in Escherichia coli, and
 RT characterization of the biologic activities of the recombinant
 RT cytokine."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF173175; AAF89833.1;
 DR InterPro: IPR000975; Interleukin_1.
 DR SMART: SM00125; IL1; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 178 AA; 20631 MW; 816D6B2B884CB497 CRC64;

Query Match 75.7%; Score 131; DB 6; Length 178;
 Best Local Similarity 70.6%; Pred. No. 2.3e-10;
 Matches 24; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKDELDGDSIMFTVQND 34
 DB 145 FLACEKERDLFKLLKKQDDNRKDSVMTVQNON 178

RESULT 5
 ID 09N1P7 PRELIMINARY; PRT; 192 AA.
 AC 09N1P7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE INTERLEUKIN-18.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RX MEDLINE=20356335; PubMed=10901174;
 RA Oem J.K., Song H.J., Kang S.W., Jeong W.S.;
 RT "Cloning, sequencing, and expression of porcine interleukin-18 in
 RT Escherichia coli."
 RL Mol. Cells 10:343-347(2000).
 DR EMBL: AF176949; AAF35169.1;
 DR InterPro: IPR000975; Interleukin_1.
 DR SMART: SM00125; IL1; 1
 SQ SEQUENCE 192 AA; 21969 MW; A51EB7AE221A16D CRC64;

Query Match 74.0%; Score 128; DB 6; Length 192;
 Best Local Similarity 70.6%; Pred. No. 6.3e-10;
 Matches 24; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 FLACEKERDLFKLLKKDELDGDSIMFTVQND 34
 DB 159 FLACEKERDLFKLLKKDELDGDSIMFTVQSKN 192

RESULT 6
 ID 09GL09 PRELIMINARY; PRT; 193 AA.
 AC 09GL09;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE INTERLEUKIN-18 (IGIF).
 GN IL-18.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN [1]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2002, 11:03:37 ; Search time 39.04 Seconds
(without alignments)
21.272 Million cell updates/sec

Title: US-09-780-035-71

Perfect score: 173

Sequence: 1 FLACEKERDLFKLIKKEDELGDRSIMFTYONED 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*

1: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*

4: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*

5: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*

6: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	173	100.0	157	2	US-08-896-605A-6
2	173	100.0	157	2	US-08-896-501A-4
3	173	100.0	157	3	US-08-884-324-1
4	173	100.0	157	3	US-08-996-338-26
5	173	100.0	157	4	US-08-558-818-1
6	173	100.0	157	4	US-08-974-469A-1
7	173	100.0	157	4	US-08-832-180-1
8	173	100.0	157	4	US-08-832-198-6
9	173	100.0	193	2	US-08-896-605A-2
10	173	100.0	193	2	US-08-896-501A-2
11	173	100.0	193	4	US-08-832-180-9
12	173	71.1	157	2	US-08-502-535B-2
13	173	71.1	157	2	US-08-908-005A-2
14	173	71.1	157	3	US-08-996-338-27
15	173	71.1	157	4	US-08-558-818-7
16	173	71.1	157	4	US-08-974-469A-7
17	173	71.1	157	4	US-08-832-180-8
18	173	71.1	157	4	US-08-832-198-11
19	173	71.1	157	4	US-09-253-523-2
20	173	71.1	157	4	US-09-251-911-2
21	53	30.6	730	1	US-08-121-713D-58
22	53	30.6	730	1	US-08-835-268-58
23	53	30.6	730	3	US-09-060-692-58
24	53	30.6	730	3	US-08-833-391-58
25	53	30.6	730	3	US-09-060-610-58
26	53	30.6	730	5	PCR-US94-10151A-58
27	50	28.9	10	4	US-08-832-198-3

28	50	28.9	244	3	US-08-750-145A-24	Sequence 24, Appl
29	50	28.9	244	3	US-08-975-698A-28	Sequence 28, Appl
30	50	28.9	244	4	US-09-417-090-28	Sequence 28, Appl
31	50	28.9	244	4	US-09-727-578-28	Sequence 28, Appl
32	47	27.2	312	1	US-08-247-908A-2	Sequence 2, Appl
33	47	27.2	312	1	US-08-453-942-2	Sequence 2, Appl
34	47	27.2	312	2	US-08-926-885A-2	Sequence 2, Appl
35	47	27.2	312	5	PCR-US94-05280-2	Sequence 2, Appl
36	47	27.2	751	3	US-08-946-026-6	Sequence 6, Appl
37	46	26.6	331	4	US-09-413-231-4	Sequence 4, Appl
38	45	26.0	1089	1	US-08-180-195-36	Sequence 36, Appl
39	45	26.0	1089	1	US-08-168-917-4	Sequence 4, Appl
40	45	26.0	1089	1	US-08-477-329-36	Sequence 36, Appl
41	45	26.0	1089	2	US-08-475-458-36	Sequence 36, Appl
42	45	26.0	1089	2	US-08-460-510-4	Sequence 4, Appl
43	45	26.0	1089	2	US-08-460-490-4	Sequence 4, Appl
44	45	26.0	1089	3	US-08-980-400-36	Sequence 36, Appl
45	45	26.0	1089	3	US-08-462-728-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-896-605A-6
Sequence 6, Application US/08896605A
Patent No. 5879942
GENERAL INFORMATION:
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,605A
FILING DATE: 18 July 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207,691/1996
FILING DATE: 19-JUL-1996
APPLICATION NUMBER: JP 156,062/1997
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TANIMOTO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-896-605A-6
Query Match 100.0%; Score 173; DB 2; Length 157;
Best local Similarity 100.0%; Pred. No. 1,5e-19;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLACEKERDLFKLLKKEDELGDRSIMFTYQND 34
Db 124 FLACEKERDLFKLLKKEDELGDRSIMFTYQND 157

RESULT 2

US-08-896-501A-4

Sequence 4, Application US/08896501A

Patent No. 5891663

GENERAL INFORMATION:

APPLICANT: TANIMOTO, Tadao

APPLICANT: KURIMOTO, Masashi

TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/896,501A

FILING DATE: 18-JUL-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 213,267/1996

FILING DATE: 25-JUL-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 31,474/1997

FILING DATE: 31-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: TANIMOTO=3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 157 amino acids

TYPE: amino acid

STRADEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-896-501A-4

Query Match 100.0%; Score 173; DB 2; Length 157;

Best Local Similarity 100.0%; Pred. No. 1.5e-19;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLACEKERDLFKLLKKEDELGDRSIMFTYQND 34
Db 124 FLACEKERDLFKLLKKEDELGDRSIMFTYQND 157

RESULT 3

US-08-884-324-1

Sequence 1, Application US/08884324

Patent No. 6060283

GENERAL INFORMATION:

APPLICANT: Takanori OKURA

APPLICANT: Kakuji TORIGOE

APPLICANT: Masashi KURIMOTO

TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE

OF INDUCING THE PRODUCTION OF INTERFERON-

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/884,324

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 185,305/96

FILING DATE: 27-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: OKURA=1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 157 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-884-324-1

Query Match 100.0%; Score 173; DB 3; Length 157;

Best Local Similarity 100.0%; Pred. No. 1.5e-19;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FLACEKERDLFKLLKKEDELGDRSIMFTYQND 34
Db 124 FLACEKERDLFKLLKKEDELGDRSIMFTYQND 157

RESULT 4

US-08-996-338-26

Sequence 26, Application US/08996338

Patent No. 6087116

GENERAL INFORMATION:

APPLICANT: TORIGOE, Kakuji

APPLICANT: OKURA, Takanori

APPLICANT: KURIMOTO, Masashi

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/996,338

FILING DATE: 22-DEC-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74,697/1997

FILING DATE: 12-MAR-1997

PRIOR APPLICATION DATA: